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1 agctataatgcggccgcata......tgatcggccgcaagcttgga 47
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                            7991742 segs, 3503743858 residues
                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                         OM nucleic - nucleic search, using sw model
                                                                                                                                              IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                  US-09-101-423B-8
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Maximum DB seq length: 200000000
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                                                                                                                                               Scoring table:
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em_esthum21:*
em_esthum22:*
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gb_est56:*
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em_esthum2:*
        em_esthum3:*
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em_estrol:
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em\_estom2:\*

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117: em_estpl6:*
118: em_estpl7:*
119: em_estpl8:*
120: em_estro14:*
121: em_estro14:*
122: em_estro16:*
123: em_estro16:*
124: em_estro16:*
125: em_estro16:*
126: qb_est59:*
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127: qb_est59:*
128: qb_est60:*
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148: qb_gss1:*
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156: qb_gss1:*
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177: em_gss1:*
178: em_gss1:*
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190: gb_gss25:*
191: gb_gss26:*
192: gb_gss27:*
193: gb_gss27:*
Pred. No. is the number of results predicted by chance score greater than or equal to the score of the results
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	ription	12834	621 zs43g09.r	2841408 T136718b	E036773 MP05D02	9//483 EST389592	EU62593 QV1	DI442/ LD40	567900 TENS	53113 zf68e	187524 EST3	E535565 601	524476 AV62	342872 1M0	1098 MgA0	51091 MgAU	710389 5070	3826 I.D131	BE976052 bs4	m	909 7070	156 7070	159 7070	5561 Tet	AV425024 AV425024 AV426457 AV426457			AV4224	5000 zp99f07.s	5803 HS_514	340//U CIIZ_I_A	UI-M-BH3	943769 UI-M-B	91371 UI-M-BH3	363902 PI1_10	58069 wi46d08.	389 yv51c08.r	009130 AB009130	20471 AV4204	144910 707013F1	E647694 UI-M	7673 fj36b05.	
SUMMARIES	DB ID	18 AI2834	4 AA236621	163 AQ841	134 BE03677	9/ AW9//483	134 BEU02	14 ANDL44	23 AT6679	1 AA06311	17 AI1875	109 BE535	37 AV624476	170 AZ342	8/ AW1810	150 AO57884	169 AZ240	7 AA438826	138 BE976	97 AW940801	40 AW1449	89 AW3314	40 AW147159	193 CNS05	36 AV425024 36 AV426457	89 AW3300	36 AV4095	36 AV4224	3 AA196000	160 AQ615	07 AWG055279	91 AW4912	137 BE943	91 AW491371	107 BE3639	24 AI76806	143 N77089	14 AB0091	36 AV42047	40 AW14491	110 BE647	39 AW07767:	
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## ALIGNMENTS

23-NOV-1998	4h93e10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone INAGE:854570 3' similar to TR:P76904 P76904 SIMILAR TO ;, mRNA	
23 - NC	clone LAR TC	
	CDNA SIMI	
EST	piens P7690	
	qh93e10.xl Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1834570 3' similar to TR:P76904 P76904 SIMILAR TC	
mRNA	C_S1 H O TR:F	
шR	_T_GB	7
313 bp	simi	92167
31	Soare 570 3'	61:3
439	10.x1 :1854	Sequence. A1283439 A1283439.1 GI:3921672 EST.
AI283439	qh93e10.x IMAGE:185	AI283439 AI283439 EST.
39	LION	ION N DS
RESULT AI283439 LOCUS	DEFINITION	ACCESSION VERSION KEYWORDS

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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 520)
Hiller, L. Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins
S., M., Hultman, M., Kucabb, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore
, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E.,
Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            zs43g09.rl Soares NHMPu_Sl Homo sapiens cDNA clone IMAGE:688000 5' similar to TR:G1079677 G1079677 LPE5P. ;, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                           Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                         1 (bases 1 to 313)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40UP from Gibco
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444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 49.8%; Score 23.4; DB 18; Length 313; 1 Similarity 73.2%; Pred. No. 31; 30; Conservative 0; Mismatches 11; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1854570"
/clone_lib="Soares_NFL_T_GBC_S1"
                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov_
                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 297.
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Unpublished (1997)
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/note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker: Site_1: Not I: Site_2: Eco RT: Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papllionoideae; Medicago.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: dcook@ppserver.tamu.edu
Other name: BSC-19-22; date: 6/8/99; Submitted to the Database of
Genome Survey Sequences (GSS) on 09/27/99; More information is
available at /http://chrysie.tamu.edu/medicago'.
                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:688000"
/clone_lib="Soares_NhHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
Tel: 314 286 1800
Fax: 314 286 1810
Email: sst@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
INAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 618 Std Error: 0.00
Seg primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 425.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49.8%; Score 23.4; DB 4; Length 520; 73.2%; Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 558)
Kim,D., Choi,H., Peng,H., Ellis,L. and Cook,DR.
BAC survey sequencing of Medicago truncatula (1999c)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genomic clone 16-K-14-022, DNA sequence.
                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                 /db_xref="GDB:5592156"
/db_xref="taxon:9606"
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The Crop Biotechnology Center
                                                                                                                                                                                                                                                                     Location/Qualifiers
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Best Local Similarity 73.2
Matches 30; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 528)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Sodai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,O.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                          Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt
, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and
Quackenbush, J.
                                                                                                   EST389592 MAGE resequences, MAGO Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE062593 528 bp mRNA EST 09-JUN-2000
QVI-BT0260-281099-023-C01 BT0260 Homo sapiens CDNA, mRNA sequence.
BE062593
                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 705)
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        patterns in a model of colon tumor
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                                                                                 02-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Assessment of gene expression patterns in a model metastasis using a 19,200 element cDNA microarray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 3528
Fax: 301 838 0208
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72.5%; Pred. No. 82;
Live 0; Mismatches 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="MAGE resequences, Note="Vector: pBluescriptSKm" 187 c 147 g 196 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
Contact: John Quackenbush
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                 mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                  AW977483.1 GI:8168734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: johnq@tigr.org
Plate: 378
                                                                              705 bp
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                                                                                                                                                                                                                                                             Homo sapiens
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Matches 29; Conserv
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                                                                          AW977483
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                                                                                                DEFINITION
                                           AW977483/C
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                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
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1. .558
/organism="Medicago truncatula"
/organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="16-r44-022"
/clone="16-r44-022"
/clone="16-rx-14-022"
/clone="16-rx-14-
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Mesembryanthemum crystallinum
Eukaryota: Viridiplantae: Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta: eudicotyledons; core eudicots; Caryophyllidae;
Caryophyllalaes, Alzoaceae; Mesembryanthemum.

1 (bases 1 to 1054)
Bohnert,H.J., Borchert,C., Brazille,S., Brooks,J., Eaton,M., Ferrea,H., Kawasaki,S., McCollough,A., Michalowski,C.B., Palacio,C.,
Functional Genomics of Plant Stress Tolerance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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BE036773
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Tel: 520-621-7982
Fax: 520-621-1697
Email: cbm@u.arizona.edu
Best blastx match: 'emblcAB38794.1| (AL035678) putative protein
[Arabidopsis thaliana] 267 9e-71'.
Insert Length: 1 Std Error: 0.00.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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/dev_stage="6 weeks"
/note=-3 d 500mM NaCl"
247 c 244 g 299 t 5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 23.2; DB 163;
Pred. No. 39;
0; Mismatches 13;
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                                                                                                                                                                                                                                                                                                                                                                 95 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1. .1054
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="MP"
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                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/done_lib="BT0200"
/dev_stage="Adult"
/note="Organ: breast; Vector: pucl8; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ONESTES PCR (U.S. Letters Patent application No. 196 .716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue manna and conna amplification were performed under low
                                                                                     (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=QV1-BT0260-281 099-023-c01&t3=1999-10-28&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 9
High quality sequence stop: 426.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó;
                                           This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Harvey,D., Hong,L., Evans-Holm,M., Pendleton,J., Su,C., Brokstein
- Low, Lewis,S. and Rubin,G.M.
BOEP/HHMI Droscophila EST Project
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI514427 625 bp mRNA EST 16-MAR-1999 LD40932.5prime LD Drsoophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD40932 5prime similar to U13637: yl FBgn0004649 PID:9535346 SWISS-PROT:P98163, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    University of California Berkeley 539 LSA, Berkeley, CA 94720-3200, USA Fax: 510 643 9947 Essistanti http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu Plate: 409 row: C column: 8
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/sex="male and female"
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/lab_host="XL1 Blue"
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/db_xref="taxon:7227"
/clone="LD40932"
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Pred. No. 96;
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High quality sequence stop: 507.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   stringency conditions.
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fruit fly.
Drosophila melanogaster
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1 Similarity 77.1%;
27; Conservative
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ORIGIN

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SOURCE

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/strain="C1-Brenner"
/db_xref="taxon:5693"
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/clone="1171"
/clone=lib="T. cruzi epimastigote normalized cDNA Library"
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/cell_type="epimastigote"
/coll_type="epimastigote"
/coll_type
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TENGO871 T. Cruzi epimasigote normalised cDNA Library Trypanosoma
Cruzi cDNA clone n442.r 5', mRNA sequence.
A1667900 GI:4826272
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AA952587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Sanchez D.O.
Instituto de Investigaciones Biotecnologicas (Univ. Nac. de Gral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.
1 (bases 1 to 267)
Verdun, R.E., Di Paolo, N.C., Urmenyi, T.P., Rondinelli, E., Frasch, A.C.C. and Sanchez, D.O.
Gene discovery through expressed sequence tag sequencing in
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                                                                                                                                                                                                                                    Score 22.2; DB 21;
Pred. No. 97;
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73.7%; Pred. No. 1.1e+02;
Live 0; Mismatches 10
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Matches 28; Conserv
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ORGANISM

KEYWORDS

REFERENCE AUTHORS JOURNAL

TITLE COMMENT

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AI187524 475 bp mRNA EST 02-0CT-2000 EST316 Manduca sexta male antennae Uni-ZAP XR library Manduca sexta CDNA clone pMSmaD85 5' similar to cuticle protein, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                               , double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pm/773 vector (Pharmacia). Library constructed by Bento Soares and W FARIMA ROMAID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterrgota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingiodea; Sphingidae; Manduca.

1 (bases 1 to 475)

Robertson, H.M., Martos, R., Sears, C., Todres, E.Z., Walden, K.O. and
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 826 Std Error: 0.00 Seq primer: -40M13 fwd. from Amersham High quality sequence stop: 253.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diversity of odourant binding proteins revealed by an expressed sequence tag project on male Manduca sexta moth antennae Insect Mol. Biol. 8, 501-518 (1999)
Other_ESTs: EST315
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/clone_lib="Manduca sexta male antennae Uni-ZAP XR
library"
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Department of Entomology
University of Illinois at Urbana-Champaign
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               252 AGCATTAATTTTGCTGCATANGCGGCCTGTTCTNCCACAA 213
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Tel: 217 333-0489
Fax: 217 244 3499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This insert is in reverse orientation. Insert Length: 1000 Std Error: 0.00
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/db_xref="taxon:7130"
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High quality sequence stop: 300.
Location/Qualifiers
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M.Fatima Bonaldo. "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46.88;
70.08;
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Matches 28; Conservative
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                                                                                                                                                            1. .447
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AI187524/c
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                                                                                                                               FEATURES
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                                                                                                                                                                                                                      Contact: Delgado Alberto
Departamento de Biologia Molecular, Lab 303
Instituto de Parasitologia y Biomedicina
Consejo Superior de Investigaciones Cientificas C/ Ventanilla No 11
, E-18001, Granada, Spain
Tel: 34 958 805058
Fax: 34 958 203323
Similar to T.cruzi elongation factor 1-gamma (mammalian homologue)
mRNA, gb|L17307|TRBEFIGHOM with Blastn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 447)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., DuBuque,T., Eavello,A., Gish,W., Hawkins
,M., Hultman,M., Kucabb,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E.,
Generation and analysis of 280,000 human expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA063113 447 bp mRNA EST U2-FEB-199, Zf68e10.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:382122 3' similar to contains element LTR5 repetitive element ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="T. Cruzi epimastigote normalised cDNA Library"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_ilu-
/clone_iltpe="alie_ilegote"
/note="Site_1: EcoRi; Site_2: NotI; cDNA library
constructed with oligo dt primed epimastigote mRNA and
cloned in pt7t318D phagemid with modified polylinker"
a 91 c 83 g 67 t
                                                                                                                                            Gonzalez Rey,E., Remisz,E., Delgado Garcia,A. and Gonzalez,A. Characterization of ESTs from Trypanosoma cruzi epimastigotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                              Trypanosoma cruzi
Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae;
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46.8%; Score 22; DB 23; Length 313; larity 73.7%; Pred. No. 1.1e+02; Conservative 0; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Trypanosoma cruzi"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="Cl - Brenner"
/db_xref="taxon:5693"
/clone="n442.r"
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1. .313
                                                                                                   Trypanosoma; Schizotrypanum.
1 (bases 1 to 313)
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                            Trypanosoma cruzi.
                                                                                                                                                                                                      Unpublished (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seg primer: T7
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nes 28; Conserv
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Query Match

Matches

RESULT 10 AA063113/c DEFINITION

g ò

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/dev_stage="newly eclosed adults and pharate adults"
//dab_host="XL1 Blue MKF and SOLK"
/note="Organ: antennae; Vector: Uni-ZAP XR; Site_1: ECORI;
Site_2: Xhoi; The library was prepared by Stratagene using
oligo-T priming and unidirectional cloning with an
adaptor at the 5' end (GGCAGGA) following the ECORI
site. The mRNA was prepared from antennae of late pupal
and newly eclosed male moths. Clones were subcloned in
vivo in mass into pBluescript maintained in SOLR cells
for DNA sequencing."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 892)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE535565 892 bp mRNA EST 09-AUG-2000 601059673F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445938 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM8417 row: b column: 19
High quality sequence stop: 612.
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46.8%; Score 22; DB 109;
Best Local Similarity 67.4%; Pred. No. 1.2e+02;
Matches 31; Conservative 0; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                        142 AGCTACGCTGCGCCAGCATACTCGGCCGCATATGCCGC 105
                                                                                                                                                                                                                                                                                                                                                                                                 1 agctataatgcggccgcatattcggcctgatcggccgc 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:3445938"
/clone_lib="NIH_MGC_10"
/cell_line="MGC36"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    255 g
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Best Local Similarity 73.7%;
Matches 28; Conservative (
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BE535565
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Chlamydomonas reinhardtii.

Chlamydomonas reinhardtii.

Eukaryota, Viridiplantee; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.

El (bases 1 to 436)

S Asamizu, E., Miura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Ohyama, K., Nakamura, Y. of Tabata, S. Generation of Expressed Sequence Tags from low-CO2 and high-CO2 adapted cells of Chlamydomonas reinhardtii

LD NA Res. (2000) In preess
Contact: Erika Asamizu

The First Laboratory for Plant Gene Research

Kazusa DNA Research Institute

Yana 1532-3, Kisarazu, Chiba 292-0812, Japan

Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="chlamydomonas reinhardtii 5% to 0.04% CO2".
/note="Vector: pBluescriptII SK-; Site_l: EcoRI; Site_2:
Xhol; The cDNA library was constructed from cells cultured
in a carbon stress acclimatized condition in which carbon
6% to 0.04%" | 16 g 94 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 558)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Slam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                     AV624476 436 bp mRNA EST 11-0CT-2000 AV624476 Chlamydomonas reinhardtii 5% to 0.04% CO2 Chlamydomonas reinhardtii cDNA clone LC078c03_r 5', mRNA sequence.
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/organism="Chlamydomonas reinhardtii"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="C9"
/db_xref="taxon:3055"
/clone="LC078c03_r"
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Contact: Robert B. Weiss
                                                                                                                                                                                                                                                          AV624476
AV624476.1 GI:10773653
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Matches 26; Conservative
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IACR-Long Ashton Research Station

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114)pblAp129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                 \mathbf{U}
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AW181098 GI:6448332
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-" /note="Vector: PWA2Inv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Keon, J.P.R., Bailey, A.M. and Hargreaves, J.A.
A group of expressed cDNA sequences from the wheat fungal leaf
blotch pathogen, Mycosphaerella graminicola
Unpublished (1999)
Contact: Hargreaves JA
Cell Biology Department
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                                                                                                                                                                                                                                                                                                                                                                                          /strain="C57Bridge"
/db_xref="taxon:10090"
/clone="UGC1M076E01"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Ascomycota incertae sedis;
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                                                                                                                                                                                                Std Error: 0.00
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1 (bases 1 to 610)
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Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                        High quality sequence stop: 558.
Location/Qualifiers
                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
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                                                                                                                                                                                                                                                                               /clone_lib="MgA Library"
//note="Vector: pSPORT1; Library constructed from cultures utilizing ammomium ions as a source of nitrogen"
a 169 c 156 g 159 t l others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 610;
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                                                                                                                                                                                     /organism="Mycosphaerella graminicola"
/strain="Strit"
/db_xref="texon:54734"
/clone="MgA0062"
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 21.8; DB 87;
Pred. No. 1.4e+02;
0; Mismatches 7;
                                                                 Email: john.hargreaves@bbsrc.ac.uk
Insert Length: 2200 Std Error: 0.00
Seq primer: M13 forward.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      564 CGACCGCGAATTCGGCTACATCGGCCGCAACCT 532
Long Ashton, Bristol, BS41 9AF, UK
Tel: +44(0)1275 392181
Fax: +44(0)1275 394281
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Best Local Similarity 78.8%;
Matches 26; Conservative (
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182.908 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                             480022 segs, 187831343 residues
                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                            - nucleic search, using sw model
                                                                                                                                                                                                               IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                              US-09-101-423B-8
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. /cgn2\_2/gcgdata/geneseq/geneseqn/NA1998.DAT:\*/cgn2\_2/gcgdata/geneseq/geneseqn/NA1999.DAT:\* /cgn2\_2/gcgdata/geneseq/geneseqn/NA2000.DAT:\*

/cgn2\_2/gcgdata/geneseq/geneseqn/Na1993.DAT:\*/cgn2\_2/gcgdata/geneseq/geneseqn/Na1994.DAT:\* /cgn2\_2/gcgdata/geneseq/geneseqn/NA1996.DAT:\* /cgn2\_2/gcgdata/geneseq/geneseqn/NA1997.DAT:\*

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Result		Query				•
No.	Score	Match	Match Length DB ID	DB	QI	Description
υ	1 43	91.5	45	18	T72784	DNA tag. Syntheti
υ	2 21.8		1503	19	V15518	Hamster oral papil
O	3 21.8		7647	19	V15519	Hamster oral papil
υ	4 21.4		42	18	T61221	Primer HUCKN.NOT f
	5 21.2		200	20	X91235	T. gondii immunoge
	6 21.2		1818		246842	Semaphorin K1 gene
	7 21.2		3481	20	X21501	DNA sequence of so
O	8 20.8		8907	21	236926	Nucleotide sequenc
υ	9 20.8		9181	20	X84323	Stealth virus nucl
1	.0 20.6		43.8 144460	21	293815	Olfactory receptor
1	1 20.4		41	15	Q70114	Lambda INNER prime
1	2 20.4		4260	6	N81768	Sequence encoding

Sequence of Mycoba Mycobacterium tube Colon cancer assoc Human alpha-2-delt Sequence of beta-9 Human alpha-2-delt Human alpha-2-delt Human alpha-2-delt Human alpha-2-delt	Porphorymonas ging Porphorymonas ging Porphorymonas ging Nebsseria gonorrho Human integrin bet Murine IL-5 cDNA g Omega-cyclohexane Trypanosoma cruzi Rifin 3193 gene. SAB virus gB glyco Nebsseria gonorrhe Neisseria meningit Escherichia coli f Haemophilus influe Human colon specif Polymucleotide seq Pseudomonas cepaci	Alpha galactosidas Alpha galactosidas Tuberous sclerosis Neisseria meningit Human normal bladd Salmonella typhimu Human heat shock p Human heat shock p	cancer; diagnosis; ds. s stranded overhang" g on complementary strand of 4 i sequence 5'-AGCT-3'"	w.
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221	20 20 20 20 118 119 21 21 118	113 116 220 221 231 18	BP. Met Met /Qua a 5, s 5, s /O14.	PS;
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υ	00 0000000	0 0 0	RESULT  172784,  XX  XX  XX  XX  XX  XX  XX  XX  XX	PA XX PI XX

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                                                                                                                                                                                                                                                                                                                                                                                                                                                   V15519 standard; DNA; 7647 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hamster oral papilloma virus.
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ID T61221 standard; DNA; 42
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                                                                       Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 29; Conserv
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                                                    Query Match
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                                                                                                                                                                                                                                            A DNA tag (T72784) having HindIII, SfiI, NotI and a defective HindIII site is used to tag human DNA from malignant, metastatic cancer calls in a novel method of screening and recovering metastasis-inducing DNA (Met-DNA). This method involves transferring the human DNA into a cell line (pref. rat Rama 37) that produces only benign, non-metastasing tumours when injected into a syngeneic animal, injecting the transformed cells into a syngeneic animal, injecting the transformed cells into a syngeneic animal, electing these animals having metastasing tumours, and recovering the Met-DNA (see also T72785-90) from them. The human DNA is tagged to assist in its removal or insertion from con into a host or vector. The tagging procedure overcomes the problem of identifying the inserted human DNA sequences in the rat genome of the transfected cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                   New isolated metastasis-inducing DNA - used to develop products to identify and treat patients at risk from metastatic tumours % \left( 1\right) =\left( 1\right) +\left( 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LI DNA; LI protein; diagnosis; papilloma virus infectious disease; cancer; screening; antitumour agent; antisense treatment; ss.
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4e-08;
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                                                                                                                                                                                Claim 6; Page 24; 38pp; English.
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Best Local Similarity 100.0
Matches 43; Conservative
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WPI; 1997-372878/34.
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DB 19; Length 1503;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 7647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer; screening; antitumour agent; antisense treatment; ss.
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                                                  Indels
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                                                                                                                               866 TATGATGCATCAGCCTTTTGATCCTGATCAGCCGCAGGTTT 826
                                                                                               4 tataatgcggccgcatattcggcctgatcggccgcaagctt 44
                                               12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diagnosis; papilloma virus infectious disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Hamster oral papilloma virus genomic DNA.
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Sequence 1818 BP; 543 A; 409 C; 359 G; 507 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA encoding an immunoglobulin (Ig), light chain, constant region. The primer can be used in a novel method for the production of recombinant antibodies, comprising the selection of B cells from a lymphocyte fraction, isolation of mRNA from individual B cells, reverse transcription of the mRNA into cDNA, amplification of the cDNA by PCR and cloning and expression of the cDNA. The recombinant antibodies can be used for diagnosis and/or therapy, while the method avoids the need for intermediate separation of light and
                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is a primer for the PCR amplification of the
                                                                                                                                                                                                                                                                                                                                      Prodn. of recombinant antibodies - by amplification, cloning and expression of cDNA generated from B-cell mRNA
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Pred. No. 8.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neavy chains and gene library screening.
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71.8%;
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                                                                                                                                                                                                                                                       Terness P, Welschof M;
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                                       DE19526546-A1.
                                                                                                                                                                                                             OPEL/) OPELZ
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                                                                                                                           20-JUL-1995;
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Synthetic.
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Best Local S
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polypeptides, or nucleic acids encoding them, can be used to modulate cellular physiology by modulating semaphorin K1 activity, e.g. semaphorin K1 polypeptide fragments or antisense nucleic acids can be used to enhance neurite outgrowth from damaged neurons. The polypeptides can also be used as immunogens, reagents for isolating other semaphorins, or as reagents for screening chemical libraries for lead pharmaceutical agents. The nucleic acids can also be used as probes and primers for diagnostic
                                                                                                                                                                                                   encode immunogenic polypeptides. The T. gondii nucleic acid molecules, immunogenic proteins and antibodies to the proteins can be used to inhibit T. gondii occyst shedding in a cat due to infection with T. gondii. They can be used for preventing T. gondii infection and for preventing the spread of T. gondii infection. They can also be used for detecting method can be used for perventing method can be used for prasalte cysts or occysts in feces, e.g. from enteric apicomplexa occysts such as Cryptosporidium occysts and Toxoplasma occysts.
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                                                                                                                                                                             The invention provides isolated Toxoplasma gondii nucleic acids that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New semaphorin polypeptides, useful cell physiology modulators and
New isolated Toxoplasma gondii nucleic acids used, e.g. to treat infection caused by this microorganism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 500 BP; 118 A; 118 C; 131 G; 133 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 21.2; |
Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 eggeegeatatteggeetgateggeegeaagett 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 17-20; 57pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Semaphorin K1 gene related sequence.
                                                                                                            Claim 4; Page 213; 381pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunogen; pharmaceutical; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.1%;
76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99JP-0065672.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0041236.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Z46842 standard; cDNA; 1818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (EXEL-) EXELIXIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-109378/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; Y56855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JP11341988-A.
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236926;
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                                                                                                                                                                                                                                    "corresponding protein sequence shown in W95020"
                                                                                                                                                                                                                                                                                            "corresponding protein sequence shown in W95019"
                   Gaps
                                                                                                                                        Sorbitol dehydrogenase; SLDH; open reading frame; ORF2; L-sorbose; D-sorbitol; vitamin C; ds.
                                                                                                                                                                                          /*tag= a
/note= "putative Shine-Dalgarno (SD) sequence for
                                                                                                                                                                                                                                                                                                                                                        /rpt_type= inverted
/note= "inverted repeat sequence IR1 as possible
transcription terminator for ORP2 gene as
indicated in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_type= inverted
/note= "inverted repeat sequence IR2 as possible
    transcription terminator for SLDH gene as
    indicated in the specification"
                                                                                                                                                                                                                                                         sequence for
                   ;
0
     DB 21; Length 1818;
                                                                                                                        DNA sequence of sorbitol dehydrogenase (SLDH) and ORF2 genes.
                   Indels
                                                                                                                                                                                                                                                                                                                             /*tag= f
/note= "mature SLDH protein sequence"
                                                                                                                                                                                                                                                        /note- "putative Shine-Dalgarno (SD)
                                        45
                  13;
                                                                                                                                                                                                                                                                                                                'note= "signal sequence for SLDH"
                               4 tataatgcggcgcatattcggcctgatcggccgcaagcttg
                                                                                                                                                                                                                             product"
                                                                                                                                                                                                                                                                                     "SLDH gene product"
                  0; Mismatches
    Score 21.2; I
Pred. No. 17;
                                                                                                                                                                                                                            "ORF2 gene
                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                        ORF2 gene"
                                                                                                                                                                                                                                                                 SLDH gene"
                                                                                X21501 standard; DNA; 3481 BP
    45.1%;
69.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98EP-0115231
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                                                                                                            21-MAY-1999 (first entry)
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                                                                                                                                                                                                                                                                                     /product=
                  Conservative
                                                                                                                                                             Gluconobacter suboxydans.
                                                                                                                                                                                                                                          .564
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                                                                                                                                                                                                              192..572
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  Query Match
Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP897984-A2
                                                                                                                                                                                                                                                                                                  sig_peptide
                                                                                                                                                                                                                                                                                                                      mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                      repeat_unit
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RBS
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                                                                   RESULT
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This represents the DNA sequence of the SLDH gene encoding a protein with sorbitol dehydrogenase (SLDH) activity. The DNA also encodes an open reading frame (ORF2) product upstream of the SLDH open reading frame, needed for SLDH activity in vivo. Host cells transformed by a vector comprising the SLDH DNA sequence are used for the recombinant expression of the sorbitol dehydrogenase. Recombinant D-sorbitol dehydrogenase is useful for producing L-sorbose from D-sorbitol. L-sorbose is an important intermediate in vitamin C production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prototype Stealth virus clone; atypically structured virus; vacuolating cytopathic effect; cytopathic virus detection; malignancy; multiple myeloma; lymphoma; brain tumour; breast cancer; salivary gland tumour; Alzheimer's disease; parkinson's disease; spongiform encephalopathy; multiple sclerosis; schizophrenia; manic depression; major depression; personality disorder; autism; Rett's syndrome; attention deficit; oppositional defiance; aggression; anorexia nervosa; bulimia; multi-system illness; virus infection; ss.
                                                                                                                                                                                                                             D-sorbitol dehydrogenase gene and recombinant protein - useful production of L-sorbose, an intermediate in vitamin {\tt C} production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated viruses, used to develop products for detection, prevention and treatment of stealth virus infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 3481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleotide sequence of the genome of Stealth virus clone 313.
                                                                           Tomiyama N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3481 BP; 674 A; 1018 C; 1001 G; 788 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                Ojima S, Shinjoh M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 gccgcatattcggcctgatcggccgcaagcttgg 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 21.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 34-37; 50pp; English.
(HOFF ) HOFFMANN LA ROCHE & CO AG F.
                                                                                                                                                                                                                                                                                                                             Claim 4; Fig 3A-D; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Z36926 standard; DNA; 8907 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.1%;
76.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26; Conservative
                                                                    Hosino T, Miyazaki T,
                                                                                                                                                                P-PSDB; W95019, W95020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-072436/06.
                                                                                                                          WPI; 1999-134646/12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stealth virus.
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236925-30 represent the nucleotide sequences of prototype Stealth virus clones. The sequences illustrate the type of sequences that can be used to generate probes and to predict antigenic and biologically active products obtainable from a viral isolate, in the methods of the invention. The specification describes tissue culture, serological and molecular based methods to detect atypically structured viruses, such as Stealth viruses, which are able to induce a vacuolating cytopathic effect (CPE) in tissue culture, and are distinguishable from Known cytopathic viruses, by appearance progression and/or host range, or by serological, electron microscopic and/or molecular markers. The products can be used for detecting viruses in patients with
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/note= "these nucleotides are represented as * in the
specification, and are included to maintain the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           specification, and are included to maintain the base numbering given in the specification"
                                                                                                                                                                                                               diseases such as a malignancy, e.g. multiple myeloma, lymphoma, brain tumours, breast cancer, salivary gland tumours, Alzheimer's disease, Parkinson's disease, spondiform encephalopathy, multiple sclerosis, schizophrenia, manic depression, major depression, personality disorders, autism, Rett's syndrome, attention deficit, oppositional defiance, aggression, anorexia nervosa, bulimia, a multi-system illness, an animal illness or an illness in a domestic dog or cat. The products can be used for detecting Stealth viruses in biological products such as blood products and foods. The products can also be used for treating or preventing virus infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a /note= "this nucleotide is represented as a * in the specification, and is included to maintain the base numbering given in the specification"
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/note= "this nucleotide is represented as a * in the
specification, and is included to maintain the
base numbering given in the specification"
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/note= "these nucleotides are represented as * in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 8907;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8907 BP; 2257 A; 2447 C; 2165 G; 2023 T; 15 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stealth virus; detection; diagnosis; infection; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stealth virus nucleic acid clone, SEQ ID NO: 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6047 GGCTGYATGGTCGGCCTGATCGGCCCCGATGGTG 6014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 ggccgcatattcggcctgatcggccgcaagcttg 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 20.8; 1
Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X84323 standard; DNA; 9181 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 44.3%;
Local Similarity 73.5%;
les 25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
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This sequence represents a Stealth virus nucleic acid clone. The invention relates to a method of detecting and characterising a stealth virus by reacting a sample suspected of containing a stealth virus with a probe from a known stealth virus and sequencing the resultant isolated nucleotide. The method comprises the steps of: (a) isolating DNA or RNA from a sample suspected of containing a stealth virus, e.g. a culture of cells showing a viral cytopathic effect; (b) testing the reactivity of the isolated DNA or RNA with a molecular probe that contains at least 18 identified from a stealth virus; and, optionally (c) sequencing the isolated DNA or RNA molecules that react with the probe. The method is used to detect stealth virus in a biological product, food or in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                determine capacity of the virus to recombine with and potentially alter the nucleic acid sequences of a cell or bacterium.
                                                                                                                       g "this nucleotide is represented as a * in the specification, and is included to maintain the base numbering given in the specification"
                                                 /note= "this nucleotide is represented as a * in the specification, and is included to maintain the base numbering given in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               environment. The method is also used to evaluate agents for their inhibitory or stimulatory effects on stealth virus replication and to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
base numbering given in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Olfactory receptor protein; olfactory; smell; receptor; binding; detection; screening; genotyping; biallelic marker; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.3%; Score 20.8; DB 20; Length 9181; 73.5%; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9181 BP; 2287 A; 2465 C; 2173 G; 2050 T; 206 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 ggccgcatattcggcctgatcggccgcaagcttg 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 19; Page 49-53; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Z93815 standard; DNA; 144460 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel strains of stealth virus
                                                                                                                                                                                                                                                                                   98WO-US27744
                                                                                                                                                                                                                                                                                                                      97US-0001184.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Olfactory receptor operon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 73.55
Matches 25; Conservative
                                                                                                                                             /note=
                                      /*tag=
                                                                                                                             /*tag=
                misc_difference 8979
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-405521/34.
                                                                                                      misc_difference 9097
                                                                                                                                                                                                                                                                                                                                                         (MART/) MARTIN W J.
                                                                                                                                                                                                               WO9934019-A1.
                                                                                                                                                                                                                                                                                   30-DEC-1998;
                                                                                                                                                                                                                                                                                                                    30-DEC-1997;
                                                                                                                                                                                                                                                  08-JUL-1999.
                                                                                                                                                                                                                                                                                                                                                                                          Martin WJ;
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Homo sapiens.

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/*tag= k
/note= "Ubiquitin 1 pseudogene complement"
complement (127489..127854)
                                                                                                                                                                                                                                                                                                               note "Ubiquitin 2 pseudogene complement"
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"Polymorphic base C or T"
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"Polymorphic base G or
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"Polymorphic base A or
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"Polymorphic base A or
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"Polymorphic base A or
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                                                                                                                                                                                                                                                                      complement (113644..114063)
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"Polymorphic base C
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"Polymorphic base A
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"Polymorphic base G
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"Polymorphic base
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"Polymorphic base
Location/Qualifiers
                                                                                                                                                      label= ORF6
10758..111564
                                                                                                                                                                                                                  32454..133389
                                                                                                                                                                                         22525..122887
                                                                                                                                                                                                                                             43398..143577
                                        /*tag= b
/label= ORF2
24851..25369
                                                                                           /*tag= d
/label= ORF4
80198..81115
                                                                                                                       '*tag= e
'label= ORF 5
                                                                                                                                                                                                                                                     /*tag= j
/label= ORF10
                /*tag= a
/label= ORF1
9711..10658
                                                                                                                                       96291..96902
                                                                     /*tag= c
/label= ORF3
                                                                                                                                                                                label- ORF7
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label= ORF8
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label= ORF9
                                                                                   15714..46661
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/note=
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/note=
141176
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Ten new olfactory receptor proteins and their biallelic markers have been described. The sequences encoding these receptor proteins and which contain the biallelic markers can be used for genotyping. The olfactory receptor proteins can be used to screen for substances which bind to them. See GENESEQ records 293816-25 and Y83386-95.
                                                                                                                                                                                                                                                                                                                                New nucleic acids encoding ten different olfactory receptor proteins and their biallelic markers, are useful in genetic analysis and in screening for compounds which bind to the receptor proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 144460 BP; 46068 A; 27088 C; 26615 G; 44676 T; 13 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21; Length 144460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enterokinase; EK; heavy chain; light chain; catalytic domain; digestive disorder; cleavage; fusion protein; trypsinogen; trypsin; enzyme; PACE gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 113793 getataagatageeteataaactgeetgaaaggeettattett 113835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44
/note= "Polymorphic base A or G" 144033
                                         /*tag= y
/note= "Polymorphic base A or G"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 gctataatgcggccgcatattcggcctgatcggccgcaagctt
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43.8%; Score 20.6; DB
Best Local Similarity 67.4%; Pred. No. 52;
Matches 29; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 103-141; 155pp; English
                                                                                                                                                                                                                                                                Bougueleret L, Malekzadeh K;
                                                                                                                                                           99WO-IB01729
                                                                                                                                                                                             98US-0104299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-MAR-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q70114 standard; DNA; 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lambda INNER primer.
                                                                                                                                                                                                                                                                                                  WPI; 2000-317933/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1994-249229/30.
                                                                                         WO200021985-A2
                                                                                                                                                                                                                              (GEST ) GENSET
                                                                                                                                                           13-OCT-1999;
                                                                                                                                                                                           14-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JAN-1993;
                                                                                                                           20-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lavallie ER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9416083-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
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                       allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
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     Qγ
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                                                                                                complementary to the lambda DNA sequence adjacent to the cloning site for the CDNA insertions (see Q70113-14). In addition, primers were designed which were complementary to the plus strand of the most 5' region of the EK coding sequence (see Q70115-16). Subcloning and sequencing provided a 116 amino acid EK heavy chain. This protein contained regions corresp. to tryptic peptides (see R57295-9).
                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence encoding Mycobacterium tuberculosis 540 and 517 AA residue
                                                                                                                                                                                                                                                           ;
0
        vectors, host cells, expression products and antibodies are useful in treating digestive disorders and for cleaving fusion
New nucleic acid encoding enterokinase activity - and related
                                                                                                                                                                                                                                   Length 41;
                                                                                        Nested oligonucleotide primers were synthesised which were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant mycobacterial peptide(s) - used in assays for diagnosis of infection, for producing vaccines and for producing antibodies
                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                   DB 15;
                                                                                                                                                                                                                                                           11;
                                                                                                                                                                                           Sequence 41 BP; 12 A; 10 C; 11 G; 8 T; 0 other;
                                                                                                                                                                                                                                                                                     5 ataatgcggccgcatattcggcctgatcggccgcaagc 42
                                                                                                                                                                                                                                                                                                   Query Match 43.4%; Score 20.4; I
Best Local Similarity 71.1%; Pred. No. 22;
Matches 27; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (3948..2395)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/label=540 AA protein
/note="P81351"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label=517 AA protein
/note="P81868"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diagnosis; assay; M.bovis; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                Example 6; Page 19; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                               N81768 standard; DNA; 4260 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88US-0159667.
87US-0019529.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88WO-US00598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..1874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Houghten R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1988-271136/38.
P-PSDB; P81351, P81868.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shinnick T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-FEB-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36-FEB-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                   29-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO8806591-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proteins.
                                      proteins
                                                                                                                                                                                                                                                                                                                                                                                                         N81768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
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δλ
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Disclosure; Fig 2a-2d; 116pp; English

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An isolated DNA molecule that consists essentially of the nucleotide sequence that corresponds to the sequence represented by position 3950 to about 2390 and from position 3948 through position 2398 of N81768 is claimed. Also claimed is a peptide sequence that consists of a 5-40 AA residue sequence that corresponds to a sequence of the 540 AA residue protein (P81351) or the 517 AA residue protein (P81868) coded for by the DNA sequence. The proteins can be used for determining previous immunological exposure of a mammal to M.tuberculosis or M.bovis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The gene was isolated by probing a lambda gtll expression library of M.tuberculosis DNA with monoclonal antibodies directed against M.tuberculosis-specific antigens. The 19kD, 71kD and the 65kD proteins and genes are claimed, and so is a vaccine comprising DNA encoding M.tuberculosis protein in a recombinant vaccine vector. P80216 is encoded on the complementary strand.
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence of Mycobacterium tuberculosis DNA contg. gene encoding 65
                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                        Length 4260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful for developing reagents for diagnosis, prevention and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genes encoding Mycobacterium tuberculosis protein antigens
                                                                                                                                                                                                                                                        6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4380 BP; 757 A; 1373 C; 1512 G; 738 T; 0 other;
                                                                                                                                                                        Sequence 4260 BP; 733 A; 1332 C; 1481 G; 714 T; 0 other;
                                                                                                                                                                                                                        6
                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                    Score 20.4; DE Pred. No. 39; 0; Mismatches
                                                                                                                                                                                                                                                                                                                      3481 tgcggccgcttgttccgcctgcgctgccgc 3510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (2398..4101)
                                                                                                                                                                                                                                                                                        9 tgcggccgcatattcggcctgatcggccgc 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shinnick TM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 12; Fig 8; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                     N80222 standard; DNA; 4380 BP
                                                                                                                                                                                                                         Query Match 43.4%;
Best Local Similarity 80.0%;
Matches 24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treatment of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192..1874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-MAR-1991 (first entry)
                                                                                                                                          for producing a vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; P80215, P80216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Husson RN, Young RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antigen; vaccine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1988-235175/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-FEB-1987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
                                                                                                                                                                                                                                                                                                                                                                                                                                       N80222;
                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                        N80222
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Gaps

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Length 4380; Indels

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This DNA sequence encodes the 65 kDa heat shock protein (see W44702), designated Mt Hsp65, of Mycobacterium tuberculosis. This protein cross-reacts with a component of articular cartilage, human Hsp60, that is up-regulated in the joints of arthritic patients. A claimed method for treating or preventing an autoimmune disease in ammmal comprises: (a) providing a particle coated with an antigen against which an immune response is mounted in the autoimmune disease. (b) delivering the particle into the recipient cell of the mammal; and (c) repeating step (b) until either a reduction in a cytotoxi immune response or a desensitizing immune response is induced in the mammal. Alternatively, step (a) comprises providing a nucleic acid construct comprising a coding sequence for the antigen of aconstruct to the recipient cell, and delivering the construct to the recipient cell, and delivering the construct to the recipient cell using a gene gun. The antigen of step (a) is selected from collagon, Mt Hsp65, mand, the recipient cell with the mand.
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     myelin basic protein, myelin oligodendrocyte glycoprotein, proteolipid protein, and epitopes thereof. These antigens mitigate cytotoxic responses and elicit antigen desensitisation. The method is used especially for treating rheumatoid arthritis or multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treatment of autoimmune diseases - by administering autoantigen-coated particles or autoantigen-encoding nucleic acid
                                                                                                                                                                                                                                                                                                                                         Heat shock protein; Mt Hsp65; autoimmune disease; immunotherapy; gene therapy; rheumatoid arthritis; multiple sclerosis; ds.
                                       0;
     Length 4380;
                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis 65 kDa heat shock protein gene.
                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= 65 kDa heat shock protein
                                     . 9
   DB 9;
43.4%; Score 20.4; D80.0%; Pred. No. 40; tive 0; Mismatches
                                                                                                        3601 tgcggccgcttgttccgcctgcgctgccgc 3630
                                                                         tgcggccgcatattcggcctgatcggccgc 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Page 55-59; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ramshaw IA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
252..1874
                                                                                                                                                                                             V05708 standard; DNA; 4380 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97WO-US09427.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0019100.
96US-0019100.
                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                    22-JUN-1998 (first entry)
                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prayaga SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AURA-) AURAGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-041892/04.
                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; W44702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W09746253-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-JUN-1996;
Query Match
Best Local Simi
Matches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haynes JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                construct
                                                                                                                                                                                                                                  V05708;
                                                                                                                                                               RESULT 14
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The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions the invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer.
                                                                                                                                                                                                                                                                                                                                                                     Cancer associated antigen; diagnosis; research; treatment; human; breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated cancer associated nucleic acids and polypeptides -isolated using sera from cancer patients, used to develop products for the diagnosis, monitoring or treatment of cancers
sclerosis. It represents a novel use for the known Mt Hsp65 gene.
                              Sequence 4380 BP; 757 A; 1371 C; 1514 G; 738 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Obata Y, Old LJ;
, Stockert E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2885 BP; 626 A; 901 C; 838 G; 520 T; 0 other;
                                                                                                          9
                                                                           DB 19;
                                                                        Score 20.4; DE Pred. No. 40; 0; Mismatches
                                                                                                                                                                    3601 tgcggccgcttgttccgcctgcgctgccgc 3630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O'Hare M, O
Scanlan MJ,
                                                                                                                                     9 tgcggccgcatattcggcctgatcggccqc 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 67; Page 651-652; 787pp; English.
                                                                                                       .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                              X40055 standard; DNA; 2885 BP,
                                                                           43.4%;
80.0%;
                                                                                                                                                                                                                                                                                                                                        Colon cancer associated gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98WO-US14679.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-0896164.
97US-0061599.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0102322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97GB-0021697
                                                                                                                                                                                                                                                                                                           02-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gure A,
Sahin U,
                                                                                                        24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    prostate cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-132448/11.
                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gout I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfreundschuh M,
                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9904265-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-JUL-1997;
10-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-0CT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-OCT-1997
10-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tureci O;
                                                                           Query Match
                                                                                                                                                                                                                                                                              X40055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen Y,
                                                                                                        Matches
                                                                                                                                                                                                               RESULT 15
X40055/c
SXS
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0; Query Match
Best Local Similarity 75.8%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps

Search completed: March 4, 2001, 12:07:09 Job time: 5664 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

March 4, 2001, 12:05:17 ; Search time 106.76 Seconds
(without alignments)
70.949 Million cell updates/sec Run on:

US-09-101-423B-8 47 Title: Perfect score:

1 agctataatgcggccgcata......tgatcggccgcaagcttgga 47 Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

280836 seqs, 80580151 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued\_Patents\_NA:\*
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*
3: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*
4: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*
5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Result No.	Score	Query	Query Match Length	DB	DI	Description
1	21.2	45.1	3481	т	US-09-136-251-1	Sequence 1, Appli
7	20.4	43.4	41	Н	US-08-200-900A-26	Sequence 26, Appl
m	20.4	43.4	41	4	4	26,
c 4	20.2	43.0	2885	e	US-08-948-705-2	2, 2
LI)	19.8	42.1	3415	1	US-08-054-077C-1	1,
9	19.8	42.1	6727	e	US-08-629-643A-5	υ,
7	19.8	42.1	6727	m	US-09-280-799-1	1,
ပ	19.4	41.3	2943	Н	US-08-042-747A-7	7,
0	19	40.4	638	Н	US-08-469-667-1	7
c 10	) 19	40.4	638	4	PCT-US95-07289-1	1,
c 11		40.0	1797	7	US-08-853-659A-28	Sequence 28, Appl
c 12	18.8	40.0	8967	7	US-08-853-659A-6	Sequence 6, Appli
13		40.0	8967	~	US-08-853-659A-9	6
c 14		40.0	8967	~	US-08-853-659A-64	64,
15		40.0	8967	7	US-08-853-659A-67	67,
c 16		40.0	24701	7	US-08-853-659A-2	7
17		40.0	24701	7	US-08-853-659A-3	'n
c 18	18.8	40.0	24701	~	US-08-853-659A-60	60,
19	18.	40.0	24701	~	US-08-853-659A-61	61,
0 20		40.0	m	m	US-09-320-878-19	19,
21	1	39.6	1708	4	PCT-US95-02481-3	3, 7
22	2 18.6	39.6		7	US-08-576-626A-2	'n
7	Н	39.1	Ψ	က	US-09-335-409-1	Sequence 1, Appli
c 24	18.	38.7		Н	US-08-278-630A-9	6
7		38.7		-1	9-601	Sequence 3, Appli
7	5 18.2	38.7		c	US-08-913-441B-3	'n
c 2	18.	38.7	1584	က	-08-907	Sequence 1, Appli
2	3 18.2	38.7	1867	7	US-08-516-801-1	Sequence 1, Appli

APPLICANT:
APPLICANT:
ATTLE OF INVENTION: CLONING OF ENTEROKINASE AND METHOD OF USE
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc. - Legal Affairs
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

ZIP: 02140

; 0

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APPLICANT: Chen, Yao-Tseng
APPLICANT: Chen, Yao-Tseng
APPLICANT: Stockert, Elisabeth
APPLICANT: Old, Lloyd J.
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ASSOCIATED WITH COLON CANCER AND METHODS FOR DIAGNOSING AND
TITLE OF INVENTION: TREATING COLON CANCER
FILLE REFERENCE: LUD-5506-JEL/NUH
CURRENT APPLICATION NUMBER: US/08/948,705A
CURRENT APPLICATION NUMBER: US/08/948,705A
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 3; Length 2885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: HEMLER, MARTIN E.
APPLICANT: RAMASWAMY, HEMAVATHI
TITLE OF INVENTION: HUMAN INTEGRIN 5 SUBUNIT PROTEIN
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43.0%; Score 20.2; D 75.8%; Pred. No. 24; ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 27-APR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/694314
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/694314
FILING DATE: 01-MAY-1991
ATTORNEY_AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-054-077C-1; Sequence 1, Application US/08054077C; Patent No. 5527679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 3425
REFERENCE/DOCKET NUMBER: 40
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
       APPLICANT: Scanlan, Matthew J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 WATER STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 3415 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: mat peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MASSACHUSETTS
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo Sapiens
US-08-948-705-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BOSTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                 2885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
                                                                                                                                                                                                                                                                                           SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                 LENGTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
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NUMBER OF SEQUENCES: 33

NUMBER READABLE FORM: MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible OFBRATING SYSTEM: PC-DOS/MS-DOS

SOFFWARE: Patentin Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 43.4%; Score 20.4; DB 4; Length 41; Best Local Similarity 71.1%; Pred. No. 11; Matches 27; Conservative 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                           SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/200,900A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PatentIn Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
43.4%; Score 20.4; DB 1;
Best Local Similarity 71.1%; Pred. No. 11;
Matches 27; Conservative 0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 ataatgcggccgcatattcggcctgatcggccgcaage 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 AGAATGCGGCCGCAAGTTCAGCCTGGTTAAGTCCAAGC 41
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                                                                                                                                                                                                                                     GI 5201-FWC
                                                                                          US/08/200,900A
                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Meinert, Maureen C.
REGISTRATION NUMBER: 31,544
REFERENCE/DOCKET NUMBER: GI 5201-F
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170 X8574
TELEPHONE: (617) 876-5851
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US94/00616
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 26, Application PC/TUS9400616 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08948705A Patent No. 6043084 GENERAL INFORMATION:
                                                                                                                  23-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 41 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 41 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: CDNA
US-08-200-900A-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
PCT-US94-00616-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT-US94-00616-26
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Gaps

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5688 AGCGAICCTCCTCTTCCTCTTCCTCCTGCTCAGCCCCAGGGGTGGA 5734
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-042-747A-7/c
; Sequence 7, Application US/08042747A
; Patent No. 5487969
                                                                                    Sequence 1, Application US/09280799 Patent No. 6136603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 57
TELECOMMUNICATION INFORMATION:
TELEPHONE: 210-554-5500
TELEFAX: 210-226-8395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Haymond, W. Bradley
REGISTRATION NUMBER: 35186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 63.89
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Mus musculus
US-09-280-799-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 112 East P
CITY: San Antonio
                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Texas: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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                                                  RESULT 7
US-09-280-799-1
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                                                                                                                                                                Gaps
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                                                                                                                          DB 1; Length 3415;
                                                                                                                                                                                                                                                                                                                                                                                                                            AUDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P. A. STREET: P. O. Box 2938
CITY: Minneapolis
STATE: MN
                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 agctataatgcggccgcatattcggcctgatcggccgcaagcttgga 47
                                                                                                                                                          12;
                                                                                                                                                                                                                                   Db 2115 ATGCCGGGGCAGAGATGGCCAGATCTGCAGCGAGCGTGG 2153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 atgoggcogcatattoggcotgatoggcogcaagcttgg 46
                                                                                                                        Score 19.8; DB; Pred. No. 35; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 42.1%; Score 19.8; D:
Best Local Similarity 63.8%; Pred. No. 39;
Matches 30; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      IL-5 TRANSGENIC MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150.167W01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FASTSEO VETSION 2.0
CURRENT APPLICATION DAY:
APPLICATION NUMBER: US/08/629,643A
                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/08629643A; Patent No. 6025539; GENERAL INFORMATION:
APPLICANT: Lee, J. L.
APPLICANT: Lee, N. A.
TITLE OF INVENTION: IL-5 TRANSGENIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/629,643
FILING DATE: 09-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 37,748
REGISTRATION NUMBER: 37,748
REFERENCE/DOCKET NUMBER: 15C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-359-3260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 5:
                                                                                                                            Query Match 42.1%;
Best Local Similarity 69.2%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 6727 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 612-359-3263
                                     CDS
337,.2733
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
   406..2733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 55402
   LOCATION:
FEATURE:
                                   ; NAME/KEY:
; LOCATION:
US-08-054-077C-1
                                                                                                                                                                                                                                                                                                         US-08-629-643A-5
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APPLICANT: Deen, Nicholas M.
APPLICANT: Karras, James G
APPLICANT: McKay, Robert
TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN-5 SIGNAL
TITLE OF INVENTION: TRANSDUCTION
FILE REFERENCE: ISPH-0340
                                                                                                                                                                                                                                                                                                                                                                                                                42.1%; Score 19.8; DB 3; Length 6727; 63.8%; Pred. No. 39; tive 0; Mismatches 17; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Eberle, Richard
APPLICANT: Berle, Darla
APPLICANT: Scinicariello, Franco
APPLICANT: Hilliard, Julia K.
TITLE OF INVENTION: Cloning and Amplification of Monkey
TITLE OF INVENTION: Virus Genes
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 agctataatgcggccgcatattcggcctgatcggccgcaagcttgga 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Cox & Smith Incorporated 112 East Pecan Street, Suite 2000
                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/280,799 CURRENT FILING DATE: 1999-03-26 NUMBER OF SEQ ID NOS: 208 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 1 LENGTH: 6727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S-0072.179
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INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: THATH: 2943 base pairs
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Gaps

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Vu, Guo-Liang
APPLICANT: Vu, Guo-Liang
APPLICANT: Rosen, Craig
TITLE OF INVENTION: Colon Specific Genes and Proteins
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
STREET: 6 Becker Farm Road
STREET: 6 Becker Farm Road
                                                                                                                                                                                                                                                                                        2 gctataatgcggccgcatattcggcctgatcggccgcaagcttgg 46
                                                                                                                                                                                                                                                                                                                    61 GCGACTACGCGGGCGTCGACTCCGGCCGCCGCGCGAGCTTGG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RILING DATE: 06-08/469,667
FILING DATE: 06-310N-1995
CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                     . Sequence 1, Application US/08469667
. Patent No. 5733748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: FERTACY, GREGOTY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 3258
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEPHONE: 201-994-1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                      MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
                                                                                                                                                                                                   Query Match
Best Local Similarity 64.49
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 638 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: mat_peptide
LOCATION: 1..501
                   single
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ZIP: 07068-1739
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                               ) NAME/KEY: CDS
; LOCATION: 87..2744
US-08-042-747A-7
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA
               STRANDEDNESS: Sir
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                             US-08-469-667-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
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GENERAL INFORMATION:
APPLICANT: Word, K.K.; Saffer, J.D.
APPLICANT: Word, K.K.; Saffer, J.D.
TITLE OF INVENTION: Of A
TITLE OF INVENTION: Of A
TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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56;
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           Sequence 1, Application PC/TUS9507289
Sequence 1, Application PC/TUS9507289
SENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Rosen, Craig
TITLE OF INVENTION: Colon Specific Genes and Proteins
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                 ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, ADDRESSEE: Stewart & Olstein STRET: 6 Becker Farm Road CITY: Roseland
                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40.4%; Score 19; 75.9%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-265
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEPHONE: 201-994-1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US95/07289
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 cgcatattcggcctgatcggccgcaagct 43
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                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 28, Application US/08853659A; Patent No. 5925522
                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Paul W. Zimmerman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 638 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 75.95
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: mat_peptide LOCATION: 1..501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                    07068-1739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 0 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                   USA
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US-08-853-659A-28/C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY:
; LOCATION:
PCT-US95-07289-1
                                                                                                                                                                                                                                                                                                               COUNTRY:
RESULT 10
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Gaps

6; Indels

15 cgcatattcggcctgatcggccgcaagct 43

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Conservative

Query Match Best Local Similarity Matches 22; Conserv

40.4%; Score 19; DB 1; Length 638; 75.9%; Pred. No. 56;

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GENERAL INFORMATION:
APPLICANT: Wong, K.K.; Saffer, J.D.
TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
TITLE OF INVENTION: Of A
TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella
                                                                                                                                                               SEQ ID NO:6 corresponds to nucleotides 15735 through 24701 of SEQ ID NO:2
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                                                                                                                                                                                                                                                                     Length 8967;
                                                                                                                                                                                                                                                                   Score 18.8; DB 2; Length 8 Pred. No. 98; 0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7996 CIGIAATGCCGGTGTTTTTTCTGCCTGATCTTCATCAA 7959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                     3 ctataatgcggccgcatattcggcctgatcggccgcaa 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Word Processor (WordPerfect 5.1) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Paul W. Zimmerman
Intellectual Property Services
Battelle Memorial Institute
PNNL P.O. BOX 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/853,659A FILING DATE: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/08853659A Patent No. 5925522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleotide
STRANDEDNESS: double stranded
TOPOLOGY: linear
                                                                                                     double stranded
                                                                                                                                                                                                                                                                     40.0%;
68.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC/XT/AT OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: none
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Washington Way
FILING DATE: n/a
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                        Best Local Similarity 68.4 Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: n/a INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 6:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Paul W. Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 8967 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington : U.S.A.
                                                                                                                                                               OTHER INFORMATION:
COTHER INFORMATION:
US-08-853-659A-6
                                                                         TYPE: nucleotide
STRANDEDNESS: dou
TOPOLOGY: linear
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US-08-853-659A-9
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                                                              LENGTH:
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APPLICANT: Wong, K.K.; Saffer, J.D.

TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection

TITLE OF INVENTION: Of A

TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella
NUMBER OF SEQUENCES: 67

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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NO:28 correspond to nucleotides 22630 through
24426 of SEQ ID NO:2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 18.8; DB 2;
Pred. No. 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DD 1101 CTGTAATGCCGGTGTTTTTTTCTGCCTGATCTTCAATAA 1064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diskette 3.50", 1.44 Mb storage
                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage
COMPUTER: IBM PC/XI/AI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 ctataatgcggccgcatattcggcctgatcggccgcaa 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Word Processor (WordPerfect 5.1) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                 SOFTWARE: Word Processor (WordPerfect 5.1) CURRENT APPLICATION DATA:
    Intellectual Property Services
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Paul W. Zimmerman
ADDRESSEE: Intellectual Property Servic
ADDRESSEE: Battelle Memorial Institute
ADDRESSEE: PNNL P.O. BOX 999
                         Battelle Memorial Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/853,659A
                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/853,659A
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US-08-853-659A-6/c
; Sequence 6, Application US/08853659A
; Sequence 5, Application US/08853659A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleotide
STRANDEDNESS: double stranded
TOPOLOGY: linear
                                    ADDRESSEE: PNNL P.O. Box 999
STREET: Washington Way
CITY: Richland
                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: n/a
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 68.4%;
Matches 26; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: none
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APPLICATION NUMBER: none
                                                                                                                                                                                                                              OPERATING SYSTEM: MS-DOS
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STREET: Washington Way
CITY: Richland
STATE: Washington
COUNTRY: U.S.A.
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MEDIUM TYPE: Diskett
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OTHER INFORMATION:
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CLASSIFICATION:
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Gaps

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APPLICANT: Wong, K.K.; Saffer, J.D.
TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
TITLE OF INVENTION: Of A
TITLE OF INVENTION: Of A
TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wong, K.K.; Saffer, J.D.

TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection.

TITLE OF INVENTION: Of A

TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella
NUMBER OF SEQUENCES: 67

CORRESPONDENCE ADDRESS:
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COMPOTER READABLE FORM:
MEDIUM TYPE: Diskette 3.50", 1,44 Mb storage
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS
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OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Processor (WordPerfect 5.1)
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/853,659A
                                                                                                                                                                                                                        Paul W. Zimmerman
Intellectual Property Services
Battelle Memorial Institute
PNNL P.O. BOX 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Paul W. Zimmerman
Intellectual Property Services
Battelle Memorial Institute
PNNL P.O. Box 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                  Sequence 64, Application US/08853659A Patent No. 5925522 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 67, Application US/08853659A Patent No. 5925522 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: nucleotide
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
US-08-853-659A-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: none
FILING DATE: n/a
INFORMATION FOR SEQ 1D NO: 64:
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STREET: Washington Way
CITY: Richland
STATE: Washington
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                          ADDRESSEE: PNNL P.O. B
STREET: Washington Way
CITY: Richland
STATE: Washington
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Best Local Similarity 68.43
Matches 26; Conservative
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TYPE: nucleotide
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US-08-853-659A-64/c
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ADDRESSEE:
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Word Processor (WordPerfect 5.1)
                                                                                                                                                                                                                                                                         Score 18.8; I
Pred. No. 98;
           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/853,659A
                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: March 4, 2001, 12:05:19 Job time: 5584 sec
                                                                                                                                                                        TYPE: nucleotide
STRANDEDNESS: single stranded
TOPOLOGY: linear
                                                                                                                            67:
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Best Local Similarity 47.4%;
Matches 18; Conservative
                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: none
                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 8967 bases
                                                                                                                          INFORMATION FOR SEQ ID NO:
                                             Unknown
                                           FILING DATE: UN CLASSIFICATION:
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US-08-853-659A-67
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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47
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em_pat:*
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gb_pr4:*
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em_pl:*
em_ro:*
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em_un:*
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44444444444444444444444444444444444444	801: 823: 843: 85:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	U57682 Rhodobacter	AL355832 Streptomy	AL022328 Human DNA	L32178 Mus cookii	M59742 Rat GABA tr	M92378 Mus musculu	M97512 Mus cookii	AE002294 Chlamydig	L38014 Bacillus Su	AC017738 Drosophil	AF012532 Bacillus	AC009915 Drosophil	299107 Bacillus su	AE003738 Drosophil	M57275 A.vinelandi	AF030293 Rathayiba	AJ002069 Rathayiba	Ul3637 Drosophila	AC015103 Drosophil	AC022365 Homo sapi.	AC011697 Drosophil
SUMMARIES	ID.	RCU57682	SCE22	HS402G11	MUSGATGABA	RATGABAT	MUSGABAX	MUSCOOK	AE002294	BACCOTJABC	AC017738	AF012532	AC009915	BSUB0004	AE003738	AVIGLNA	AF030293	RRAJ2069	DMU13637	AC015103	AC022365	AC011697
	DB	7	29	52	11	11	11	11	٦	7	59	Н	55	7	30	7	Н	7	32	58	62	26
	% Query Match Length DB	96898	25458	177241	2042	4054	4074	4402	10908	2013	17103	18622	101962	213190	226159	1950	2565	2565	6254	14724	151673	218971
	% Query Match	52.8	49.8	49.8	48.9	48.9	48.9	48.9	48.9	48.1	48.1	48.1	48.1	48.1	48.1	47.2	47.2	47.2	47.2	47.2	47.2	47.2
	Score	24.8	23.4	23.4	23	23	23	23	23	22.6	22.6	22.6	22.6	22.6	22.6	22.2	22.2	22.2	22.2	22.2	22.2	22.2
	ult No.	П	7	m	4	Ŋ	9	7	æ	6	10	11	17	13	1.4	15	16	17	18	19	20	21
	Result No.	ຸ່່ວ	υ						U	υ		Ö		υ		υ	O	υ	υ	O	υ	

<b>-</b>	Direct Submission Submitted (O'MAY-2000) Streptomyces coelicolor sequencing project, Submitted (O'MAY-2000) Streptomyces coelicolor sequencing project, Dayid A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK  Notes: Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics Details of S. coelicolor sequencing at the Sanger Centre are available on the World Mude Web.  (UBL: http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system egy SCPB7.01c. SC (S. Coelicolor). TB7 (Cosmid name). Oll (first CDS), c (complementary strand).  The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The more significant similarity to other CDS in the database. The length in codons is given for each CDS.  The more significant similarity to other CDS in the database. The length in codons is given for each CDS.  The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon.  Gene prediction is based on positional base preference in codons using a specially developed Hidden Markow Model (Krogh et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp./  jun/cgl-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon of the sequence (optimally 5-13bp before the mitiation codon). If this cannot be identified we choose the most unstream initiation codon. This sequence (optimally 5-13bp before the initiation codon. If may be shorter because we only sequence overlapping sections once, or longer, because we only sequence overlapping sections once, or longer because we only sequence of mail overlap between neighbouring submissions.	restriction fragment. Location/Qualifiers 125458 /organism="Streptomyces coelicolor A3(2)/strain="A3(2)" /db_xref="taxon:100226" /clone="cosmid E22" complement(1490) /gene="SCE22.01c" complement(<1490)
ACCESSION VERSION KEYWORDS SOURCE ORGANISM AUTHORS TITLE JOURNAL MEDILINE REFERENCE AUTHORS JOURNAL REFERENCE AUTHORS JOURNAL REFERENCE AUTHORS AUTHOR	TITLE JOURNAL COMMENT	FEATURES source gene CDS
AE003495 Drosophil AE004219 Vibrio ch E15110 gDNA encodi E15111 Whole seque AE004529 Pseudomon AP001516 Bacillus L29299 Frankia aln AC01766 Drosophil AC010066 Homo sapi AC010066 Homo sapi AC010356 Drosophil AC010357 Neisseria AL096877 Streptomy U00667 Ovis aries D38228 Xanthomonas AX000291 Sequence U18243 Alcelaphine AF035940 Pseudomon AF005370 Alcelaphine AF035940 Pseudomon AF05370 Alcelaphine AF053928 Mus muscu	BCT 07-FEB-1997  -43-147, complete sequence.  subdivision; Rhodobacter group;  corn,R.  orn,R.  ein, MGCB, Univ of Chicago, 920 E.  capsulatus"  f the complete encyclopedia"  f the complete and 1 others  53 t 1 others  bb 2; Length 86896;  hes 7; Indels 0; Gaps 0;	552 BCT 10-MAY-2000
22.2 47.2 308373 30 AE003495 2.2 46.8 11936 1 AE004219 21.8 46.4 1503 81 E15110 21.8 46.4 1627 1 AE004582 21.8 46.4 300950 2 AE001516 21.8 46.4 300950 2 AE001516 21.6 46.0 119526 54 AC010516 21.6 46.0 119526 54 AC010564 21.6 46.0 119526 54 AC010506 21.6 46.0 119526 54 AC010906 21.6 46.0 341319 30 AE003536 21.4 45.5 11489 1 AE003536 21.4 45.5 11489 1 AE003536 21.4 45.5 35437 29 SCTH2 21.2 45.1 11874 79 AHUISH216 21.2 45.1 2557 29 XANAG4C 21.2 45.1 11874 79 AF005370 21.2 45.1 11874 79 AF005370 21.2 45.1 11806 879 AF005370 21.2 45.1 11806 79 AF005370 21.2 45.1 11802 73 AE32828	RCU57682 86896 bp DNA U57682.  RROdobacter capsulatus cosmids 143-11 U57682.  U57682.  U57682.  RROdobacter capsulatus.  RROdobacter capsulatus.  RROdobacter capsulatus  RROGOBACTERIA  1 (bases 1 to 86896)  Rumar, V. Fonstein, M. and Haselkorn, Bacterium genome sequence  Nature 381 (6584), 653-654 (1996)  2 (bases 1 to 86896)  Ponstein, M., Kumar, V. and Haselkorn, Bacterium genome sequence  Nature 381 (6584), 653-654 (1996)  2 (bases 1 to 86896)  Ponstein, M., Kumar, V. and Haselkorn, Burcer Submission  Direct Submission  Sibmitted (07-MAY-1996) M. Fonstein, Sibth, Chicago, IL 60637, USA  Location/Qualifiers  // Corganism="RB1003" // Ab_Arref="taxon:1061" // Ab_Arref="taxon:1061" // Map="cosmids 143-147 of the 15089 a 28056 c 28787 g 14963 t  tch 52.88; Score 24.8; DE  tch 52.88; Score 24.8; DE  tch 52.88; Pred. No. 50;  29; Conservative 0; Mismatches	11 cggccgcatattcggcctgatcggccgcaagcttgg 46
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 RUG15 82/C DUCUS DEFINITION R ACCESSION U VERSION VERSION U VERSION U VERSION U VERSION U VERYORDS R REFERENCE 1 AUTHORS F TITLE B JOURNAL N AUTHORS F TITLE D JOURNAL S SOURCE AUTHORS F TITLE D JOURNAL S SOURCE AUTHORS F TITLE D JOURNAL S SOURCE AUTHORS F AUTHORS S SOURCE SOURCE SOURCE OUGHY MATCH BASE COUNT ORIGIN OUGHY MATCH BEST LOCAL	Oy 11 Db 76687 RESULT 2 SCE22/C LOCUS DEFINITION

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    107
/note="nominal overlap with Streptomyces coelicolor cosmid
SCE87"

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VPWQEQALMSWAGLRGAVP11LATIPMVEGVAGSHR1FNIVFVLVVYYLLVQGPFLPW
LARKIRLGKGDEAADLGIESAPLERLRGHLLSVTIPEGSRMHGVEVNELRLPTGAAVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="wastvtrpgygollrtrgawtfllpgfaarQpfawlflsivllv
Qhttgsygdaadaavtgyswavfapfsgrlabrggravllbevluhtryb
AldaplwalflaavptgasypQvgpwyrarwavglkopflwstaraaresytdblffy
LGPLVATALCTAVDPAGLVTFBAALTLVGGLLFAARKSTEPKVGSADGGHARVBHYSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLVYLAIGVAMGODGIGDIQFDNAELVQVIGYGALVVILAEGGLGTKWKEAKPALPAA
SALALGGVAVSVGVTAAGAHYLTGLEWRQALIVGAVVSSTDAAAVFSVLRRIPLPKRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVVRDGTSFVPLPTTGLRRGDELLVVATDPVRDAAEARLRAVGHGGKLAGWLGTGGTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MRCARERERPLTVHHLNOLLLVCSLVLLIAVAAVRISSRSGLPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLKHVALPASGLYPIAVMSIAIAAYAAGAMAHGSGFLAVYLASMVMGNARLPHWPATR
                                                                                                                                                                                                                                                                                                                         /product="putative secreted penicillin acylase (fragment)"
/protein_id="CAB90968.1"
/db_xref="GI:7799504"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAYWSISTVRASFPQTKGSITLDGLSGPVDVKRDGYGIPQVYASTEEDLFWAQGYVQA
QDRFYEMDVRRHWTAGRLSEWFGKSQIDNDEFLRTLGWHRVAKKEYDEKLSDSTKKYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGTLEAESGFNDAPVVILVVAFSTAGPIEHWYVLLGEIALELAIGAAIGLAVGWLGSW
                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MPPTTTASTGQQAGTSGRKKARKGRKGRLLVLVLVLALIGGLAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="SCE22.02 possible Na+/H+ antiporter, len: 515 aa; similar to TR:09XAD9 (EMBL:AL.079348) Streptomyces scalicolor putative Na(+)/H(+) antiporter SG6f3.14c, 514 aa; fasta scores: opt: 1828 z-score: 1992.7 E(): 0; 55.18 identity in 497 aa overlagh Contains Pfam match to entry PF00999 Na. H. Exchanger, Sodium/hydrogen exchanger family and possible hydrophobic membrane spanning regions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="SCE22.03, possible ABC transporter integral membrane protein, len: 421 ad; similar to TR:050532 (EMBL:AL009204) Streptomyces coelicolor hypothetical 41.1 kD protein SC9B10.25c, 393 aa; fasta scores: opt: 721 z-score: 787.1 E(): 0; 34.7% identity in 383 aa overlap. Contains match to Prosite entry PS00211 ABC transporters family signature and possible hydrophobic membrane
/note="SCE22.01c, possible secreted penicillin acylase (fragment), len: >162 aa; similar to C-terminal region of SW:PAC2_PSES3 (EMBL:M18278) Pseudomonas sp. penicillin acylase II precursor (EC 3.5.1.11) Acyll, 773 aa; fasta scores: opt: 291 z-score: 347.5 E(): 6.8e-12; 39.18 identity in 110 aa overlap. Contains possible N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 856. 2007
/gene="SCB22.02"
/hote="FCB2 match to entry PF00999 Na_H_Exchanger,
Sodium/hydrogen exchanger family, score 73.90, E-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_table=11
/product="putative ABC transporter integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="putative Na+/H+ antiporter"
/protein_id="CAB90969.1"
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                                                                                                                                                                                                                      signal peptide sequence"
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/gene="SCE22.03"
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/gene="SCE22.03"
                                                                                                                                                                                                                                                            /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             805. .2352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="SCE22.02"
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gene CDS

gene

CDS

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similar to TR:005574 (EMBL:29452) Mycobacterium tuberculosis hypothetical 11.4 kD protein MTC1237.05c, 110 as fasta scores: opt: 379 z-score: 372.3 E(): 2.8e-13; 52.3% identity in 10? as overlap. High content in serine amino acid residue in C-terminal domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="mankvkaelgvlggsgfysflddvtevrudtpygppsdslflge
vagrrvafldrhgrghhlpphrlnyranlwalrsvgarqvlgpcavgglrpeygpgtl
Lvpdgfvdrtrsrpstyfdglpmpdgtvpnvvhvsladpycptgraalkaargrewe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the gene for a novel protein similar to Xenopus gamma tubulin
interacting protein (yeast SPC98 homolog), the gene for a novel
protein similar to yeast and bacterial predicted proteins, the gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
LRVPGVRVLIVAFLGIGSVFGGMQVSLAAFTESIGEPGLNGVLYGVFAAGNMISGLAC
GAJAMKVAPGORELLVGYAALALTASGLAAAHSVLVLAGLGLLVGMCVAPAIVTGYTLV
EDLVPAGARTERAFTHLTGAVALGQAAAVTVAGQLEDRFRDGAGFLVPMGGTVLALAVL
VALRSRLATRSHGRTVARGVGHRAPATVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phosphorylase, len: 280 as; similar to TR:CAB49985
(EMBL:AJ248286) Pyrococous abyssi methylthioadenosine
phosphorylase related (MapP), 265 as; fasta scores: opt:
Til z-score: 861.9 E): 0, 43.4% identity in 265 as
overlap and to SW:MTAP_HUMAN (EMBL:U22233) Homo sapiens
5-methylthioadenosine phosphorylase (EC 2.4.2.28)
(MTAPASE) MtaP_S3 as; fasta scores: opt: 653 z-score:
791.7 E(): 0, 38.2% identity in 254 as overlap. Contains
pfam match to entry PF00896 Mtap_RNP, phosphorylases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HS402G11 177241 bp DNA PRI 12-DEC-1999
Human DNA sequence from clone RP3-402G11 on chromosome
22q13.31-13.33 Contains the MAPK12 gene for mitogen activated
protein kinase 12 (SAPK3), the MAPK11 gene for mitogen activated
protein kinase 11 (FRKM11), gene KIAA0315, the gene for a novel
protein similar to KIAA0901 and mouse histone deacetylase MHDA2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="putative methylthioadenosine phosphorylase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                        /note="SCE22.04, hypothetical protein, len: 110 aa;
                                                                                                                                                                             'note="PS00211 ABC transporters family signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 25458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="serine amino acid residues rich region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="SCE22.05, possible methylthioadenosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="hypothetical protein SCE22.04"
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/db_xref="GI:7799507"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 24364 GCTGTTCGCGCCGGATAGCCGACCTGTGGGGCCGCAAGC 24324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 gctataatgcggccgcatattcggcctgatcggccgcaagc 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.8%; Score 23.4; DB 29; 73.2%; Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="CAB90972.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4397. .5239
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                                                                                                                      3660. .3704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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Best Local Similarity
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/note="L2 repeat: matches 2630. .2643 of consensus"

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http://www.sanger.ac.uk/fdp/Christon can be found at During sequence assembly data is compared from overlapping clones. Muring sequence assembly data is compared from overlapping clone to together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with nortation and to the overlapping clone, as we submit sequences with corresponding to the overlapping clone, as we submit sequences with a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Bm:. BMBI: Sw:. SWISSPROT: Tr:. TREMBL: WP: WORNPEP: Information on the WORNPEP database can be found at
                                                                                                                                                                                                                                            HTG: CpG island; GB110; KIAA0315; KIAA0901; kinase; MAPK11; MAPK12; Mitogen activated protein kinase; mitogen-activated; MOV10; MRS1; PRKM11; SAPK3; SPC98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    true
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire, CEB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk replaced in 29, 1999 this sequence version replaced gi:5262835.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
for a novel protein similar to C. elegans F38A5.2, the gene for a novel protein similar to MRS1 and the gene for a novel protein similar to mouse MOV10 (GB110) and yeast and plant predicted proteins. Contains ESTs, GSSs and fifteen putative CpG islands,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP3-402G11 is from the library RPCI-3 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacapac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence is the entire insert of clone RP3-402G11 The true right end of clone RP5-89814 is at 23403 in this sequence. The tright end of clone RP11-232E17 is at 56734 in this sequence. The true right end of clone RP4-600024 is at 96013 in this sequence. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .243 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat: matches 2643. .2747 of consensus"
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/note="AluSp repeat: matches 1. .300 of consensus"
3073. .3086
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/note="AluSq repeat: matches 1. .306 of consensus"
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note="Alusx repeat: matches 1. .298 of consensus"
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/note=_AluSx repeat: matches 1. .312 of consensus"
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/note="MER58 repeat: matches 170.
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/db_xref="taxon:9606"
/chromosome="22"
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/clone="RP3-402G11"
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                                                                                                                                                                                                                   AL022328.21 GI:5263010
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Coville, G.
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2775. .3073
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                                                                                                                                               complete sequence.
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// 10.00="M.K. repeat: matches 32. .247 of consensus" 18590. .18727 repeat: matches 38. .247 of consensus" 18590. .18727 repeat: matches 389. .525 of consensus" 21238. .2188 // 1.2188 // 1.2188 // 1.2188 // 1.2215 // 1.2245 // 1.2245 // 1.2245 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 // 1.2246 //
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/note="L1 repeat: matches 2915. .3769 of consensus"
24501. .24747
/note="L1MEc repeat: matches 1501. .1751 of consensus"
24978. .25194
/note="L1MEc repeat: matches 272. .492 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="AluSg/x repeat: matches 133. .302 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="MER46C repeat: matches 113. .337 of consensus"
18366. .18558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Ally repeat: matches 1. .303 of consensus" 9848 .10020 .10020 .10020 .10046 .10034 .10036 .10034 .10016 .10034 .10019 .10034 .10019 .10034 .10019 .10039 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10019 .10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "note="AluJo repeat: matches 30. .150 of consensus"
1543. .9847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             // note="MERAC repeat: matches 1. .22 of consensus" 14063. .14370 // note="Alux repeat: matches 2. .310 of consensus" 15488. .15718 // note="Alux repeat: matches 51. .295 of consensus" // note="Alux repeat: matches 91. .296 of consensus" 16816. .17110
                                                      .527 of consensus"
                                                                                                                                                                                                                                                                   .308 of consensus"
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/note="L1 repeat: matches 3780. .3926 of consensus"
23516. .23691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="AluSx repeat: matches 1. .294 of consensus" 9427. .9542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Alusg repeat: matches 1. .296 of consensus" 11227. .11641
/note="MER4C repeat: matches 22. .461 of consensus" 11642. .11957
/note="Alux repeat: matches 1. .310 of consensus" 11958. .11981
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18096. .18300
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                                                                                                                                                                                                                                                                                                                                                                                                           // Consensus 1. .303 of consensus 7218. .7516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="AluY repeat: matches 1. ,309 of consensus"
                                                                                                                                                             .303 of
/note="AluJo repeat: matches 29. 6406. .6907
/note="match: GSS: Em:AQ475194"
                                                                                                                                                       'note="AluJb repeat: matches 77.
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DTWKGRFDFLMSCVGYAIGLGNVWRPPYLCGKNGGGAFLIPYFLTLIFAGVPLFLLEC
SLGQYTSIGGLGVWKLAPMFKGVGLAAAVLSFWLNIYYIVIISWAIYYLVNSFTTTLP
                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MATDNSKVADGQISTEVSEAPVASDKPKTLVVKVQKKAGDLPDR
DTWKGRFDFLMSCVGYAIGLGNVWRFPYLCGKNGGGAFLIPYFLTLIFAGVPLFLLEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLGQYTSIGGLGVWNVAPMFKGVGLAAAVLSFWLNIYYIVIISWAIYYLYNSFTTTLP
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Guastella,J., Nelson,N., Nelson,H., Czyzyk,L., Keynan,S.,
Miedel,M.C., Davidson,N., Lester,H.A. and Kanner,B.I.
Cloning and expression of a rat brain GABA transporter
Science 249 (4974), 1303-1306 (1990)
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0
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M59742.1 G1:204221
GABA transporter; gamma-aminobutyric acid transporter. Rat brain, cDNA to mRNA, clone GAT-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
48.9%; Score 23; DB 11; Length 2042;
Best Local Similarity 68.1%; Pred. No. 3.6e+02;
Matches 32; Conservative 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                  /note="gamma-aminobutyric acid transporter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1814 AGATATTGTGCGCCTGAGAATGGCCCTGAGCAGCCGCAGGCTGGCA 1860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                         /product="GABA transporter"
/protein_id="AAA37663.1"
/db_xref="GI:533226"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAA63487.1"
/db_xref="GI:204222"
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150. .1949
                                                                                     /tissue_type="retina"
/tissue_lib="lambda ZAP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10116"
/clone="GAT-1"
   /organism="Mus cookii"
/db_xref="taxon:10098"
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                                                         /dev_stage="adult"
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JOURNAL
MEDLINE
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VERSION
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2042)
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/note="AluSx repeat: matches 1. .288 of consensus"
33999. .34144
/note="LIMEc repeat: matches 2231. .2385 of consensus"
27926. .28225
/note="AluSx repeat: matches 2. .302 of consensus"
28634. .28937
/note="AluSy repeat: matches 1. .304 of consensus"
29001. .29119
/note="AluJo/FLAM repeat: matches 3. .133 of consensus
29659. .30170
/note="Libit repeat: matches 5189. .5489 of consensus"
30171. .30449
                                                                                                                                                                                                                                                         Gaps
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GABA transporter; gamma-aminobutyric acid transporter.
Mus cookii (library: lambda ZAP) adult retina cDNA to mRNA.
Mus cookii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="AluSg repeat: matches 1. .310 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35626. 35922
/note="Alusg repeat: matches 1. .297 of consensus"
35932. 36042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49.8%; Score 23.4; DB 52; Length 177241; 73.2%; Pred. No. 1.4e+02; tive 0; Mismatches 11; Indels 0; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ruiz, M., Egal, H., Olan, X.J., Sarthy, V.P. and Sarkar, H.K. Cloning, expression and localization of a mouse retinal gamma-aminobutyric acid transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus cookii GABA transporter (GAT-1) mRNA, complete cds L32178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34792, .34910
/note="7 copies 17 mer 73 conserved"
35157, .35466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34781. .34916
/note="4 copies 34 mer 86 conserved"
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Query Match

Matches

MUSGATGABA LOCUS DEFINITION

RESULT

ORGANISM

VERSION KEYWORDS SOURCE

ACCESSION

REFERENCE AUTHORS

TITLE

Location/Qualifiers 1. .2042

Unpublished (1994)

JOURNAL

FEATURES

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Gaps

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/note="hypothetical protein; identified by Glimmer2;
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426. .1016
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              ATÁWULVYFCIWKGVGWTGKVVYFSATYPYIMLITLFFRGYTLDGARGGILFTTTPIN

FRLSDSEWWLDAATQIFFSYGLGLGSLIALGSYNSFUNNYRDSIIVCCINSCTSMFA

GFVIFSIVGEMAHVTKRSIADVAASGEQLAFLAAYPEAYTOLTSLIANJILFFGMLLML

GIDSOFCTVEGFTATUVDEY PRILIRNRELFTAAVCISTLGLSTTTQGGTVYFKLF

DYYSASGMSLLELVFFCVSISWFYGNNRFYDNIQEWYGSRPCIWWKLCWSFFPIIV

AGVFLFSAVQWTPLTMGSYVFFKWGQGVGWLMALSSWVLIFGYMAYMFLTLKGSLKQR

LQVMIQPESDINRPENGPEQPAGSSASKEAYI"

AG11. 4036

/gene="Gaba transporter"

a 1119 c 980 g 1070 t
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WKQCDNPWNTDRCFSNYSLVNTTNMTSAVVEFWERNMHQMTDGLDKPGQIRWPLAITL
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 4074)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 4402)
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Mus musculus (library: cDAN lambda-zap) brain cDNA to mRNA.

Mus musculus
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A family of genes encoding neurotransmitter transporters
Proc. Natl. Acad. Sci. U.S.A. 89, 6639-6643 (1992)
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Pred. No. 3.3e+02;
0; Mismatches 15; Indels (
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Mus musculus GABA transporter mRNA sequence.
M92378
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/tissue_lib="cDAN lambda-zap"
1..4074
                                                                                                                                                                                                                                                                                     0; Mismatches
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/product="GABA transporter"
| 1115 c 995 g 1077 t
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Matches 32; Conservative C
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Read, T.D., Brunham, R., Shen, C., Gill, S.R., Heidelberg, J.F.,
White, O., Hickey, E.K., Peterson, J., Umayam, L.A., Utterback, T.,
Berry, K., Bass, S., Linher, K., Weidman, J., Khouri, H., Craven, B.,
Bowman, C., Dodson, R., Gwinn, M., Nelson, W., DeBoy, R., Kolonay, J.,
McClarty, G., Salzberg, S.L., Eisen, J. and Fraser, C.M.
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Chlamydia muridarum, section 26 of 85 of the complete genome.
AE002294 AE002160
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Liu,Q.-R., Mandiyan,S., Nelson,H. and Nelson,N.
A family of genes encoding neurotransmitter transporters
Proc. Natl. Acad. Sci. U.S.A. (1992) In press
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                               Length 4402;
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/db_xref="taxon:83560"
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
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Submitted (01-MAR-2000) The Institute for Ge
Medical Center Dr, Rockville, MD 20850, USA
Location/Qualifiers
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68.1%; Pred. No. 3.3e+02;
iive 0; Mismatches 15
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1090 c 1230 g 1
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us-09-101-423b-8.rge

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CDS

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SIANTERSLRSEEVLHSQSLLRQKELFPNTSNIKKELPNTKSILHTPLNRRSPSGSD
DDVYYTPRAGLSSAFTSALGDISGISSSSTSSKTSTPKAKRRVVRSSRSERNARHRR
KEDHRQNQEESSDDEDSSPLESPRRKKYRSRFK"
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AHFFETAMISCKNYRALSNWITVEFAGRCKATGKTLPFTGILPEWVAQLVNFIDRGVI
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NGKAKALGFLVGQIMKRIFGKAPPKRVNELLLAAMRDA"
COMPIEMENT (9731. . 10834)
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MODRYARSKEGFGKEVTRRILLGGVYLSAERGOHIFYKKGTAVRATLLEAFOSAFECC
DVIAMPVCASPAIRDTDVLDPVSLYLQDIYTVAVNIA*IPAISVPSGLSKEGLPLGVO
FIGKRGADQQLCQVGYSFQEHSQIKQLYPRAVNGLFDGGME"
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SARFCPIALGSDTGGSIRQPAAFCGVVGFKPSYGAVSRYGLVAFGSSLDOIGPLTTVV
EDVALAMDAFAGRDIKDATTRDFFRGTFSQALSLEVPKLIGVPRGFLDGLQEDCKENF
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PIVRGCCVRAIVEGEEKTFELAQTHLEDDAGMLKHFGDFAGVDYNRAGVPLIEIVSKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CKERALLRASRIDDKLAKGDPIGILAGIPIGVKDNIHITGVKTTCASKMLENFVAPFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MGIAHTEWESVIGLEVHVELNTASKLFSPARNHFGDEPNTNISP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MVKIMAPITPTTSPQVKGLLSRFLTAPDRHPKLRYVYDISLIAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'translation="MYRKSALELRDAVVNREISVTAITEYFYHRIESYDEQIGSFLSL
                                                                                                                                                                                                                                                                                                                                                                                                                       VAIDISDIILEATVHHFVGPEDLREDMVTSDFTREEFLANVPVSLGGLVKVPTVIK"
                                                                                                                            putative; identified by match to TIGR protein family HMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="glutamyl-tRNA(Gln) amidotransferase subunit A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="glutamy1-tRNA(Gln) amidotransferase subunit
/protein_id="AAF39140.1"
/db_xref="GI:7190312"
                                                                                                                                                                                                                                 /product="glutamyl-tRNA(Gln) amidotransferase subunit putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to PID:1653395; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="similar to GB:AL009126; identified by sequence
                                                                                                 /note="glutamyl-tRNA(Gln) amidotransferase subunit C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="conserved hypothetical protein; identified by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="conserved hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3251 t
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/db_xref="G1:7190313"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(9731. .10834)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAF39139.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity; putative"
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/codon_start=1
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/transl_table=11
                                                                                                                                                                                                                              /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="TC0271"
/5707. 8102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
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/gene="TC0272"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5707. .8182
/qene="TC0271"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8184. .9650
/gene="TC0272"
                                     6393. .6695
/gene="TC0270"
                                                                                                                                                                                            /codon_start=1
/gene="TC0270"
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SVEGAGHSSRGIFGRLQAGLGRLARRVGEAVRNTVGSIFPQRAGAEQRTGKARTKYSP
SASRGLRLMFTDFWRYRVLHRNPPMDGLFAKLDADEAEDMAAYTKEYVSNLEKRGAAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MLCKVCRGLSSLIVVLGAINAGILGATGYRVNIVARLLGEGTML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NPLFFTNNSALNGGAICCINBONLSEKGCLSLAYNOETLFSGNSAKEKGGAIYTKHMV
LRHNGPVSFVNNSAKLGGAIAIQSGGSLSIIAGGGSVLFQNNSCHFSDQGTVRNAIYL
EKNALLSSLEARHGDILFFDPIVQEVVSPEFSTTSALTPLRIQTNTNRAVIFSSENLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DGPGVSKLSEVDTGFWLDMEKLSDAVLSANIOKGLRARFVLNOSIPQLESLEERFRKL
ESACDEARASLKEAGWIKEGKEPNKAQRAFRRFVEESRNLELSFGSFGESARRLSARV
SQGLAAAGEAIRRCFDCRKGKYSLKKDLSSEELNLAEELIRFTDEMGIERDPDGNYNI
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PPRSSLNYETPRFREYDVPRNSARSYYDVPRVPPQNEVEEMHVTKGMRSSVYACFVAG
                                                                                                                                                              /db_xref="G1:7190307"
/translation="MVCPLQGCGLLRSEASGSSSEEVNQDPLLDAISYSVRVCLAVAK
                                                                                                                                                                                                                              HTESAKIYHQNRKRCHKVGCWGKVKRFLCCCCCAEKEWVEGKITGLGLWMQEHIRLHG
LITGYAVHLLEGVCWERMLLAGETLSPEDQRQLNAALENSSITWMRLMLDSSDGKVDG
LESPAMQEDLFAQYREKVGIGNLADAVALRHFCNRT"
complement(1104. .3707)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MRPDHVNLCCLCATILSPTAILFGQDALDKSALITKNPNSIVCT
FLEDCTMENFSPALLSHARQDDPLYIIGNTHNWFVSNLHPSTNEERFLKEKGDLSIQD
FRFLSFTDCSSSTEDSPSILYHKNGQLFLRNNGNMSFYRNHSEGSGGALSTDALFLQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEEKTEANLISKIQQPIELQSGCLVLKDRVILSAPSLSQAPQALLVMDVGTSLTTSSD
LKLTTLSIPLHSIDTENSVSIQSPTLSIQKIFLSNSEHENFYENVELLSKDQKDIPLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLPKGLPHPDLPDGNLSSHFGYQGDWNFSWQTSDQRETLVANWTANSYIPHPERQSAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VANTLWNTYSDMQAVQSMINTTAQGGAYLFGTWGSAVSNLFYSHGNSGKSTDNWKHRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGYLFGISTHSLDDHSFCLAAGQLFGKSSDSFVTSADTTSYIAAIQTQIATSLIKISA
QACYNESIHELKTKYRSFSKEGFGAWHSVAVSGEIGASIPIVSNGSGLFSSFSIFSKL
QGFSGKQDGFEESRGEARAFADSSFTNISLPVGIAFEKKSQKTRNYYHFLGAYIQDLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RCVESGPVTLLKNSVTWDAPMANLDSRAWMFRLTNQRALHRFQTLVNMSYMLRGQSYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NY LFTNFEENSSAKNGGAIQAQTLSLSRNVSSLSFSRNRANLNGGAICCQNLICSGNV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to GP:4376270; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="hypothetical protein; identified by Glimmer2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="polymorphic membrane protein G family" /protein_id="AAF39136.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TQAAXVVAGIAGVIAFLNFFKCCFKKRHSDCCSSKGGCHHHTDRE"
6393. .6695
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/protein_id="AAF39137.1"
/db_xref="G1:7190309"
                                                                                                 /product="hypothetical protein"
/protein_id="AAF39135.1"
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/db_xref="GI:7190310"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity; putative"
/codon_start=1
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/gene="TC0268"
3956. .5800
/gene="TC0268"
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Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
1 (bases 15361 to 18622)
Henriques.A.O., Beall, B.W., Roland, K. and Moran, C.P. Jr.
Characterization of cotJ, a sigma E-controlled operon affecting the
polypeptide composition of the coat of Bacillus subtilis spores
95286532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (10-DEC-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA
This sequence was identified as CDM:10211936 by the submitter. For more information on this record e-mail to fly@celera.com.
* NOTE: This is a "working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 17103)
Adams.M. and Venter, J.C.
                                                                                                  14; Indels
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                                                                                                                                                                                         3 ctataatgcggccgcatattcggcctgatcggccgcaagcttgga 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 agctataatgcggccgcatattcggcctgatcggccgcaagcttg 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
3705 c 3714 g 4573 t
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68.9%; Pred. No. 3.8e+02;
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                                           DB 2;
                                     48.1%; Score 22.6; DB 2
68.9%; Pred. No. 5e+02;
.ive 0; Mismatches I
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Borriss, R. and Schroeter, R.
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Drosophila melanogaster,
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HMEQFSPMEALRKGTLWKDLYDFYENPYRGGDAHGKKG"
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Bacillus subtilis cotJABC operon, polypeptide(s) affecting spore
coat composition, cds.
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Bacillus subtilis
Bacteria: Firmicutes: Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
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1. .2013
7. organism="Bacillus subtilis"
/strain="168"
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/db_xref="GI:1377749"
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/db_xref="GI:1377751"
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/gene="cotJB"
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SAFAEFERDMIVERTQEGKMLAKQNPDFREGRPKKFTKQQINHALTILLENHSYKQVED
MTGISVSTLVRAKKKKAAEAING"
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enthyltransferase: SwissProt Accession Number P55135;
similar to Chlamydia trachomatis Homl: SwissProt Accession
Number P55137"
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//gene="yeff"
/note="similar to Enterococcus faecalis plasmid PY117 orf4
encoded by GenBank Accession Number D78257"
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hypothetical protein MJECS02 encoded by GenBank Accession
Number L77119"
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Submitted (03-JUL-1997) Borriss R., Humboldt University, Institute
of Biology, Chausseestrasse 117, Berlin, Germany, D-10115
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The 55-58 degree segment of the Bacillus subtilis chromosome, region spanning from the purA gene cluster to the cotJ operon Unpublished
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/db_xref="G1:2318067"
/translation="AKKRLRRSPPADNCGDEAEAGSVCVL"
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/strain="168 trpC2"
/db_xref="taxon:1423"
/map="55 to 58 degree"
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/db_xref="G1:2318060"
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/db_xref="G1:2318059"
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/gene="yefB"
complement(227. .1129)
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1. .18622
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                                                                                                                                                                   3 (bases 1 to 18622)
Borriss, R.
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505. .4159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="
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                                                                                                                                                                                                                                                                                                                                                                                                                       source
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AUTHORS
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                                                      TITLE
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PASGKSRALMFIGLDKLINQGLRKVIVAVPERSIGSSFKNTDLKSYGFFENWKVDPRN
NLTVGGDNSKVKSFVRFMESDDQVLICTHSTLRFAFEKIDDKAFDNCLLAIDEFHHVS
ADVNSRLGELLRSIIHNSSAHIVAMTGSYFRGDSVPILLPEDBELFDKVTXSYYEQLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GYEYLKGFGIGYHIYOGQYTSAINEVLDTNKKTIVHIPNVNSGESTKDKYDEVGKILD
MIGEWEXQDDDTGIIYVKRHSDGKTLKIADLVDDQVGRENVVAYLRNIEALDDLDIII
ALGMAKEGFDWPFCEHTLIVGYRGSLTEIVQIIGRCTRDSYNKTYAQFTNLIAMPDAK
DEVYYTVHTWILKAISASLLAMEQVLIERFRRRRESEKSSTFGELFVKGKERFSTE
NVKKIIENDINDLKAKTCKIHKSKTFGGEVDRYVLNKYLIPKVIQKVYPNLSDEEIEE
VRQHVVLDTVWKGAKSEVVGSKEFIRMADKFINIEDLDINLIDSINPFQKAFEVLSKE
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/db_xref="GI:2318063"
/translation="MASNRYHSINEIMESQLFYQITTPPKKTQKAQYDPEVEKFLEII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RCIFENGTESDMLLRSLSAELYKHGRRVTDNEDTLLDNVREDDVSTGFIYVLKSLSTD
PQISSIKNLYKIGFTTGSVENRIRNAENQSTYLYAPVEIVTTYQVFNMNASKFETAIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                TNAKVAEVSTNSVTQGEQVSILANDELEKFGIQINFANKSEKWANNAKNNAAVIVVIVG
FGPLDTKVNKYLFVDETKKLVSNISPYLTDGENILVSSRTK PISDLFKLHFGRMPNDG
GGLLFTTEYTDAINKYPELVPFKKRFTGSVEFINGGLRYCLANLNEAKFEKIKSNPLI
GERISISKNHREKSTDKGINTLTPWKRFTGYPHETTNYSIVVPSVSSENRFY FPMGLA
GADTILSNLIYVIYADEIYLLGILMSNHMTWYKAVARKIKTDKYRYSAGLCYNTFPIP
ELSTRRKNEIEBAILLEILDLREEQGGTLAELXNPSTMPIELKVAHEKLDGIVERAYRO
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                                                                                                                                                                                                                                                                                        LDKNERDDVPSYLKEFPYVNGQLFTEPHTELEFSAKSRKLITECGELLNWAKINPDIF
GSMIQAVASEBSRSYLGMHYTSVPNIMKVIKPLFLDKLNQSFLDAYDDYTKLENLLTR
IGKIKFFDPACGSGNFLITTYKELRRMEINIIKRLQELLGEYLYVPSVTLSQFYGIEI
                                                                                                                                                                                                QNLTKRVGEVHLKNKVWFKEAKKGKLFDALIDIEQQVEYLSAKPRYLLVTDYDGVLAK
DTKTLEALDVKFEELPQYFDFFLAWKGIEKVEFEKENPADIKAAERFARIYDVLRKEN
                                                                                                                                                                                                                                                                                                                                                                                          EDFAHDVAKLSLMIAEHQMNEELKNEVHNAVRPTLPLHTAGDIRCANAIRVEWTEVCP
AQGSEEVYYFGNPPYLGSKKQNKEHKSDMLSIFGKVKNGKMLDYISAWFYFGAKYAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MENIIEINYNQTGKSKKTNEYGMREMQARAFEKRNSQYLLVKAP
                                                                                                                                                                                                                                                             NIIETNRGLDLFLIRLLFCFFAEDTDIFKRNSFTNLIKTLTEEDGSNLNKLFADLFIV
                                                                                                                                                        /translation="MALIDLEDKIAEIVNREDHSDFLYELLGVYDVPRATITRLKKGN
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complement(7490. .8180)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAB66475.1"
/db_xref="GI:2318062"
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/protein_id="AAB66477.1"
                                                                                           /protein_id="AAB66474.1"
/db_xref="G1:2318061"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KOFESDEERLEVLLKLYQEMTER"
4152. .4161
/gene="yeeB"
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/transl_table=11
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/transl_table=11
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/codon_start=1
/transl_table=11
                                                                /product="YeeA"
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/gene="yeeB"
4171. 5967
/gene="yeeB"
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/gene="yeeC"
6064. .7228
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6080
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/gene="yeeC'
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gene

CDS

RBS

gene

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TITLE
JOURNAL
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E I (bases 1 to 101962)
S Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G., Butenhoff,C., Champe,M., Chavez,C., Chew,M., Clesiolka,L., Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L., Hinkle,A., Hoskins,R.A., Hummasti,S.R., Karra,K., Kearney,L., Lee,B., Lewis,S., Li,P., Ling,H., Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S., Pfeiffer,B., Richards,S., Sethi,H., Svirskas,R.R., Wan,K.H., Webster,D., Sequencing of Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MPAGVPYNAVNGVTLKEGLQKFAKVILPKPYGTSSSGRRTPAPH
VPPVTVKYGEHFARWSRKKVLKPNIIYKTKEGYTYTTDNYGRITSVKADLQLGEAKRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QYAQTNAGKPQDRKPDDDGGHLIATQFKGSGQFDNIVPMNSQINRSGGKWTEMDRAG
ACLSKRPPKKVAVQIEPVYSGDSLRPSYFDVTYKIGSRKEISVSIKISLGVRRMETRR
MQDLYQLIGEKLNDIIPGEMYKIYLFASVLDDSTWVLFHFRTPENNQIIYSQDIPSHY
NVSKQIFKTLLRELEELFEELFEERTHNNDDVWTNITLTLDRSGEFQLDYNYDDILAS
ELDGYERIATWEYKNLGILPEDEDDKEFVISYLGL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="similar to Bacillus subtilis orf94 hypothetical
59.7 kDA protein in CWLA-CISA intergenic region: SwissProt
Accession Number P45942"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC009915 101962 bp DNA HTG 10-FEB-2000
Drosophila melanogaster chromosome 3 clone BACR09L14 (D751) RPCI-98
09 L 14 map 94A-94A strain y; cn bw sp, *** SEQUENCING IN PROGRESS
                               'translation="MTVRKELIKQINLTITVIKTINQKNPTPMVKNILKRYEEAKEFI
                                                       LQSSDGKFEEDLSKVRNKLDTLTRAYLESANDYMNPMLKEMHKTEKLLKEYDETTQS"
                                                                                                                                                                  /note="rho independent terminator; deltaG= -10.2kcal/mol"
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Cathiker,S.E., Apbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G.,
Butenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L.,
Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48.1%; Score 22.6; DB 1; Length 18622; ilarity 68.9%; Pred. No. 3.7e+02; Conservative 0; Mismatches 14; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 17005 CCAAAATGAGGTCCAATATGCAGCAGCAGCCGCAAACTCTGA 16961
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                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAB66478.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (9541. .10791)
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                                                                                 complement(8175. .8180)
                                                                                                                                                                                                                complement(8308. .9470)
/gene≈"yeeE"
                                                                                                                                                                                                                                                                                complement(8308. .9417)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(9464. .9470)
/db_xref="GI:2318064"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="GI:2318065
                                                                                                                                                                                                                                                                                                                                                                                           /transl_table=11
/product="YeeE"
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/codon_start=1
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HTG; HTGS_PHASE1.
fruit fly.
                                                                                                                                                                                               /citation=[2]
                                                                                                                /gene="yeeD"
8277. .8298
                                                                                                                                                                                                                                                                                                                /gene="yeeE"
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Best Local Similarity
Matches 31; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ***, 84 ur
AC009915
                                                                                                                                        terminator
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Matches
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KEYWORDS
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Direct Submission

Direct Submission

Submitted (08-28P-1999) Drosophila Genome Center, Lawrence Berkeley, Laboratory, MS 64-121, Berkeley, CA 94720, USA

On Feb 11, 2000 this sequence version replaced gi:6598737.

For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdqp@fruitfly berkeley.edu. All contigs in this submission meet the following cutoffs: length >= 200 bases.

* NOTE: This is a "working draft' sequence record is a sonists of 84 contigs. The true order of the pieces arbitrary. Gaps between the contigs are represented as true of N. but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will
Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Poon, L., Sequelira, A., Sethi, H., Snir, E., Syliskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             contig of 1017 bp in length
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of 1001 bp in length
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gap of unknown length
contig of 942 bp in length
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gap of unknown length
contig of 1197 bp in length
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of 741 bp in length
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of 805 bp in length
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of 1342 bp in length
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of 1548 bp in length
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of 1792 bp in length
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of 2543 bp in length
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                      unknown length
of 1620 bp in length
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of 1083 bp in length
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of 900 bp in length
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of 853 bp in length
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Kunst, F., Ogasawara, N., Moszer, I., Albertini, A.M., Alloni, G., Azevedo, V., Bertero, M.G., Bessieres, P., Bolotin, A., Borchert, S., Azevedo, V., Bertero, M.G., Bessieres, P., Bolotin, A., Borchert, S., Borriss, R., Boursier, L., Brans, A., Braun, M., Brignell, S.C., Garter, N.M., Choi, S.K., Codani, J.J., Connerton, I.F., Cummings, N.J., Canter, N.M., Choizot, F., Devine, K.M., Dusterhoft, A., Entlich, S.D., Emmerson, P.T., Entian, K.D., Errington, J., Fabret, C., Ferrari, E., Foulger, D., Fritz, C., Fujita, M., Fujita, Y., Fuma, S., Galizzi, A., Galleron, N., Ghim, S.Y., Glaser, P., Goffeau, A., Golightly, E.J., Gardi, G., Guly, B.J., Haga, M., Haibert, H., Holsappel, S., Hosono, S., Hullo, M.F., Itaya, M., Jones, L., Joris, B., Karamata, D., Kasahara, Y., Khaerr-Blanchard, M., Klein, C., Kobayashi, Y., Koetter, P., Koningstein, G., Krogh, S., Kumano, M., Neulado, R.P., Lardinois, S., Lauber, J., Lazarevic, V., Lee, S. M., Levine, A., Liu, H., Maxuo, M., Moestl, D., Medigue, C., Medina, N., Mellado, R.P., Mizuno, M., Moestl, D., Maxai, S., Noback, M., Noone, D., O'Reilly, M., Ogawa, K., Ogiwara, A., Oudega, B., Park, S. H., Parro, V., Pohl, T. M., Portetelle, D., Porwollik, S., Prescott, A.M., Presecan, E., Pujic, P., Rivolta, C., Rocha, E., Roche, B., Rose, M., Sadaie, Y., Sato, T., Sekowska, A., Seror, S.J., Serror, P., Shin, B.S., Soldo, B., Sekowska, A., Seror, S.J., Serror, P., Shin, B.S., Soldo, B.,
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Pred. No. 3e+02;
0; Mismatches 14; Indels 0;
                                                                                                                       jor...
g of 741 bp in length
of unknown length
ig of 530 bp in length
of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 62414 AGCGATCAGGCGTTCGCCTGTTCGCCCAGCTCCGTGGAAAGTTTG 62458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus subtilis
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
1 (bases 1 to 213190)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contig of 512 bp in length gap of unknown length contig of 590 bp in length gap of unknown length contig of 865 bp in length gap of unknown length
                                                  on are inknown length y of 739 bp in length inknown length
                                                                                                                                                                                                                                                                            unknown length
of 586 bp in length
unknown length
of 648 bp in length
unknown length
of 841 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contig of 388 bp in length
gap of unknown length
contig of 450 bp in length
gap of unknown length
   unknown length
of 433 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 agctataatgcggccgcatattcggcctgatcggccgcaagcttg 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of 450
i unknown lens
of 531 bp in lens
m length
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Z99107 AL009126
Z99107.1 GI:2632866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 48.1
Best Local Similarity 68.9
Matches 31; Conservative
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VERSION
KEYWORDS
SOURCE
ORGANISM
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BSUB0004/c
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DEFINITION
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join(2610. 2954,3074. 3091)
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KGLAQLALQTLDERARELGAERLALHVFAHNETAVYLYQKMGYAMTNIRMRKQLC"
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LIGGETABGGSVWYSPSANIGYLTQEVFDLPLEOTPBELFENETEKARGHVQNLMRH
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TLHLIHNDLAPAQGQILRKDIKLALVEQETAAYSFADQTPAEKKLLEKWHVPLRDFH
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GLASWSEKAHAQSTKKEGFKEYHRVKAKRTDAQIKSKQKRLEKELEKAKAEPVTPEYT
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3117. .3590
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Sorokin, A., Tacconi, E., Takaqi, T., Takahashi, H., Takemaru, K., Takeuchi, M., Tamakoshi, A., Tanaka, T., Terpstra, P., Tognoni, A., Tosaco, V., Uchiyama, S., Vandenbol, M., Vannier, F., Vassarotti, A., Viari, A., Wambutt, R., Wedler, E., Wedler, H., Weitzenegger, T., Winters, P., Wipat, A., Yamamoto, H., Yamane, K., Yasumoto, K., Yasumoto, K., Yoshikawa, H. F., Zumstein, E., Yoshikawa, H. and
                                                                                                                                                                                                                                                                                                                                                                              Submitted (18-NOV-1997) I. Moszer, A. Danchin, Institut Pasteur, Regulation de l'Expression Genetique, 28 rue du Docteur Roux, 75724 Paris Cedex 15, FRANCE. E-mail: moszer@pasteur.fr, adanchin@pasteur.fr Phone: +33 (0)1 45 68 84 41, Fax: +33 (0)1 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MIELEVVIRTVASFGLLLIAERILGKQTISQMTIFDFIAAITLG
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                                                                                                                                                                                        The complete genome sequence of the gram-positive bacterium
                                                                                                                                                                                                                                                                                               2 (bases 1 to 213190)
Kunst, F., Ogasawara, N., Yoshikawa, H. and Danchin, A.
Direct Submission
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33. .740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="168"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="ydfs"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="ydfs"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="ydfT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="ydgA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .213190
                                                                                                                                                                                                                    Bacillus subtilis
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                                                                                                                                                                  Danchin, A
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                                                                                                                                                                                                                                                                            MEDLINE
                                                                                                                                                                                                                                                                                                     REFERENCE
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Db 154579 CCAAAATGAGGTCCAATATGCAGCATGAGCAGCCGCAAACTCTGA 154535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
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           Baxendale, J., Bayraktaroglu, I., Beasley, E.M., Beeson, K.Y.,
Benos, P.V., Berman, B.P., Bhandari, D., Bolshakov, S., Borkova, D.,
Botchan, M.R., Bouck, J., Brokstein, P., Burtis, K.C.,
Busam, D.A., Butler, H., Cadleu, E., Center, A., Chandra, I.,
Cawley, S., Dahlke, C., Davenport, L.B., Davies, P., de
Pablos, B., Delcher, A., Deng, Z., Mays, A.D., Dew, I., Dietz, S.M.,
Dodson, K., Doup, L.E., Downes, M., Dugan Rocha, S., Dunkov, B.C.,
Dunn, P., Durbin, K.J., Evangelista, C.C., Ferraz, C., Ferriera, S.,
Fleischmann, W., Fosler, C., Gabrielian, A.E., Garg, N.S.,
Fleischmann, W., Fosler, C., Gabrielian, A.E., Gorgell, J.H., Gu, Z.,
Gelbart, W.M., Glasser, K., Glodek, A., Gong, F., Gorrell, J.H., Gu, Z.,
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Wei, M.H., Ibeywam, C., Jalali, M., Kalush, F., Karpen, G.H., Ke, Z.,
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Li, J., Li, Z., Liang, Y., Lin, X., Liu, X., Mattei, B., McIntosh, T.C.,
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Muzny, D., M., Nelson, D.R., Nelson, K.A., Nixon, K.,
Nusskern, D.R., Pacleb, J.M., Palazzolo, M., Pittman, G.S., Pan, S.,
Pollard, T., Puri, V., Reses, M. G., Reinfart, K., Remington, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adams,M.D., Celniker,S.E., Holt,R.A., Evans,C.A., Gocayne,J.D., Amanatides,P.G., Scherer,S.E., Li,P.W., Hoskins,R.A., Galle,R.F., George,R.A., Lewis,S.E., Richards,S., Ashburner,M., Henderson,S.N., Sutton,G.G., Wortman,J.R., Yandell,M.D., Zhang,Q., Chen,L.X., Sutton,G.G., Wortman,J.R., Yandell,M.D., Zhang,Q., Chen,L.X., Barandon,R.C., Rogers,Y.H., Blazej,R.G., Champe,M., Pfeiffer,B.D., Wan,K.H., Doyle,C., Baxter,E.G., Helt,G., Nelson,C.R., Gabor Miklos,G.L., Abril,J.F., Agbayani,A., An,H.J., Andrews-Pfannkoch,C., Baldwin,D., Ballew,R.M., Basu,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AE003738 AE002708
AE003738.2 GI:10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota;
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Pollard,J., Puri,V., Reese,M.G., Reinert,K., Remington,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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YWFCWISIAMADLTAVGLYTQYWLPGVPQWYPGLIALIILLIMNLATYKLFGELEFWF
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AFVGIELVGLTAGETENPEKVIPKAINNIPVRVLLFYIGALLVIMSIYPWDIINPSES
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/gene="ydgF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="ydgF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="similar to amino acid ABC transporter (permease)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          function="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                226159 bp
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Pred. No. 2.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 213190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-OCT-2000
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/db\_xref="FLYBASE:FBgn0038935" db\_xref="FLYBASE:FBan0007087" 97395. .87481,88000. /gene="CG7087"

88077,88145.

.>88261)

/product="CT21905"

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REFERENCE
AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA
mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Simpson, M., Skupski, M.P., Smith, T., Spier, E., Spradling, A.C., Venter, E., Wang, R., Sun, E., Svirskas, R., Tector, C., Turner, R., Venter, E., Wang, A.H., Wang, X., Wang, Z.Y., Wassarman, D.A., Weissenbach, J., Williams, S.M., Woodage, T., Worley, K.C., Wu, D., Yang, S., Yao, Q.A., Ye, J., Yeh, R.F., Zaveri, J.S., Zhan, M., Zhang, G., Zhao, Q., Zheng, L., Zheng, X.H., Zhong, F. N., Zhong, W., Zhou, X., Zhu, S., Zhu, X., Smith, H.O., Gibbs, R.A., Myers, E.W., Rubin, G.M. and Venter, J.C. The genome sequence of Drosophila melanogaster science 287 (5461), 2185-2195 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          On Oct 9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saunders, R.D., Scheeler, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rockville, MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20196006
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                                                                                                                                                                                                                                                                                                                                                                        GKNSVGKELTSNSSESLSNSSSKSQLNKRPSSSSSISPIKHPHRNYRNRMRYTATEPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .226159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000 this sequence version replaced gi:7300816. Location/Qualifiers
                                                                                                                            EVMAPYQSDNSQTLGDLLLSFLHYYSVFDYGKYAISIRVGGVLPIEVCRAATAPKNDI
                                                                                                                                                                                                                                                      EMRRPPKVMGCKNKWDPLSLSVWKKFLESQQTRHVYKIKMRLWRAIYTVAMKNYPRYG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Celniker, S.E., Gibbs, R.A., Rubin, G.M. and Venter, C.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
.84568,84948.
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      .85351,85825.
      .85931
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COMMENT

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gene
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EEDEIYGFGYGVFAPRVARGGLTQQQQLLQQQTLQTQQSIQQQQQQQQQQQQQQQLPIVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLKTVNRRDRNNQQNGAQARAANDRLRHFQMINGGAGGQQHSFEETIHRQQKQSHTRR
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87395. 87481,88000. 88077,88145. 88261)
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KEYWORDS
SOURCE
                                     BASE COUNT
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
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                                     424
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agctataatgcggccgcatattcggcctgatcggccgcaagcttg 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glutamine synthetase
J. Bacteriol. 172 (11),
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Azobacter vinelandii DNA.
Azotobacter vinelandii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Toukdarian, A., Saunders, G., and Kennedy, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.vinelandii glutamine synthetase (glnA) gene, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecular analysis of the Azotobacter vinelandii glnA gene encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 68.9
31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 1950)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .1 GI:142308
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478. .18
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

RESULT 1 AI283439/c LOCUS DEFINITION

ACCESSION VERSION KEYWORDS AI283439 313 bp mRNA EST 23-NOV-1998 qh93e10.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:1854570 3' similar to TR:P/6904 P76904 SIMILAR TO ;, mRNA sequence. AI283439 AI283439.1 GI:3921672 EST.

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MEDLINE
COMMENT
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1 (bases 1 to 520)

Hillier, L. Lennon, G., Becker, M., Bonaldo, M. F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, N., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA236621 520 bp mRNA EST 07-AUG-1997 zs43g09.rl Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:688000 5/similar to TR:G1079677 G1079677 LPESP. ;, mRNA sequence.
                         Washington University School of Medicine
                                                        Contact: Wilson RK
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Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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1 (bases 1 to 313)
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                         Genome Res. 6 (9), 807-828 (1996)
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Seq primer: -400P from Gibco
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHLl9W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
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/clone_lib="Soares_NFL_T_GBC_S1"
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/db_xref="taxon:9606"
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                                                                                      Plate: 409 row: C column: 8
High quality sequence stop: 507.
                                                                                                                                                                                                                                                                                         BDGP/HHMI Drosophila EST Project
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 625)
                                                                                                                       Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: 409 row: C column: 8
                                                                                                                                                                       539 LSA, Berkeley, CA 94720-3200, USA Fax: 510 643 9947
                                                                                                                                                                                                                  G. M. Rubin-Molecular and Cell Biology University of California Berkeley
                                                                                                                                                                                                                                                                    Contact: Harvey, D.
                                                                                                                                                                                                                                                                                                                                         Harvey,D., Hong,L., Evans-Holm,M., Pendleton,J., Su,C., Brokstein
,P., Lewis,S. and Rubin,G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster
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This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fruit fly.
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization
                                                                 Location/Qualifiers
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pregnant uterus"
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
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AW977483 705 bp mRNA EST389592 MAGE resequences, MAGO Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mesembryanthemum crystallinum Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Eukaryota; Caryophyllidae; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Alzoaceae; Mesembryanthemum.
                                                                                                                                                                                                                                                                                                                                                                                      Email: cbm@d.arizona.edu
Best blastx match: 'emb|CAB38794.1| (AL035678) putative protein
[Arabidopsis thaliana] 267 9e-71'.
Insert Length: 1 Std Error: 0.00.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bio Sciences West room 513, Tucson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Michalowski, C.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 520-621-7982
Fax: 520-621-1697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             University of Arizona
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/dev_stage="6 weeks"
/note="3 d 500mM NaCl"
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/clone_lib="LD Incoophila melanogaster embryo pOT2"
/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
/lab_host="%Il Blue"
                                                                                                                                                                                                                                                                                                               /organism="Mesembryanthemum/db_xref="taxon:3544"
/clone_lib="MP"
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BE062593
                                                                                                                                                                                                                                                                                              Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Ragai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOllveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Fax: +55-11-2/0/002
Email: asimpson@ludwig.org.br
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human
This sequence was derived from the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quackenbush, J. Assessment of gene expression patterns in a model metastasis using a 19,200 element cDNA microarray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 705)
Hegde, P., Qi, R., Abernathy, K., Dharap, S.,
I.E., Saeed, A.I., Sharov, V., Lee, N.H., Y.
                                                                                                                         Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 528)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: johng@tigr.org
Plate: 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 301 838 3528 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: John Quackenbush
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
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AW977483.1
                                                                                                                                                                                    Contact: Simpson A.J.G.
                                                                                                                                                                                                                                         sequence tags
                                                                                                                                                                                                                                                          Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                          Tel: +55-11-2704922
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/note="Vector: pBluescriptSKm"
187 c 147 g 196 t
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72.5%;
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Pred. No. 74;
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                                     Cancer Genome
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                                                                                                                                 Paulo-SP,
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: dcook@ppserver.tamu.edu
Other name: BSC-19-22; date: 6/8/99; Submitted to the Database of
Genome Survey Sequences (GSS) on 09/27/99; More information is
available at 'http://chrysie.tamu.edu/medicago'.
                                                                                                                                                                                                                                                                                                                                                                  Department of Plant Pathology and Microbiology, Rm 120 L.F. Peterson Bldg, College Station, TX 77843-2132, USA Tel: 409 845 8743 Fax: 409 862 4790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kim,D., Choi,H., Peng,H., Ellis,L. and Cook,DR. BAC survey sequencing of Medicago truncatula (1999c) Unpublished (1999)
                                                                                                                                                                                                                                               Class: BAC subclone.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Texas A&M University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Cook DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Medicago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Medicago truncatula
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 558)
                                                                                                                                                                                                                                                                   primer: pUC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Crop Biotechnology Center
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          /Clone_lib="shotgun sub-library of BAC clone 16K14"
/note="Vector: pUC18; BAC survey sequences were obtained from sheared BAC DNA subcloned into the Smal site of pUC18. The template DNA for sequencing was obtained by PCR using universal primers. Sequencing reactions were primed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196.,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         stringency conditions."
180 c 152 g
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/clone="16-K-14-022"
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/db_xref="taxon:9606"
/clone_lib="BT0260"
                                                                                                                                                             /organism="Medicago truncatula"
/cultivar="genotype A17"
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the PUC-C primer site (CAGGAAACAGCTATGACCATGATTACGA)
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Pred. No. 86;
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W06254.1 GI:1278977
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73.7%;
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Local

BASE COUNT

REFERENCE AUTHORS

VERSION

KEYWORDS ACCESSION

ORGANISM

DEFINITION

AQ841408 RESULT

COMMENT

JOURNAL

FEATURES

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444 TGCTAGCTTGTGGCTGCACAGGCTTTATAAGGGGAAGCATTAT 486
81 AATCCACACTTGCCGAAGATCCGGTGGACGATGCGGCC 118
                                                     1 aatccaagcttgcggccgatcaggccgaatatgcggcc
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Dietrich,N., Dubuque,T., Hillier,L., Kucaba,T., Wan,K.L.
Waterston,R.H. and Boothroyd,J.
WashU-Merck-Stanford-NIH Toxoplasma EST project
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WashIngton University School of Medicine
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: toxo@watson.wustl.edu
David Sibley at toxoest@borcim.wustl.edu for further information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TgESTzy78d04.rl TgRH Tachyzoite cDNA Toxoplasma gondii cDNA clone tgzy78d04.rl 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  relating to organism, clone or library availability.
                                                                                                                                                                                                                                                                   /note="Voctor: Lambda ZAP; Site_1: EcoRI; Site_2: XhOI; /note="Voctor: Lambda ZAP; Site_1: EcoRI; Site_2: XhOI; /note="Voctor: Lambda ZAP; Site_1: EcoRI; Site_2: XhOI; /note="Voctor: Lambda ZapI victor: The library was constructed by K.I. Wan, Cambridge University. cDNAs were synthesized from polyA RNAs by oligo d(T) priming and directionally cloned into the EcoRI to XhOI sites of the Lambda ZapII vector using the ZAP-CDNA synthesis kit (Stratagene). WARRING: the library contains a small percentage of cDNAs derived from the human host cells." a 66 c 78 g 83 t 3 others
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1 76 c 95 g 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="tgzy78d04.r1"
/clone_lib="TgRH Tachyzoite cDNA"
/lab_host="XL1-Blue MRF'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:5811"
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                                                                                                                                          Score 22;
Pred. No.
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Pred. No. 86;
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96;
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RESULT 10
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AA952587/c
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Contact: Delgado Alberto
Departamento de Biologia Molecular, Lab 303
Instituto de Parasitologia y Biomedicina
Consejo Superior de Investigaciones Cientificas
, E-18001, Granada, Spain
                                                                                                                                                                                                                                                                                                                  A1667900 313 bp mRNA
TENGO871 T. Cruzi epimastigote normalised cDNA Library Trypanosoma
ruzi cDNA clone n442.r 5', mRNA sequence.
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Tel: (54-1)752-9639 or (54-1)752-0021
Fax: (54-1)752-0021 or (54-1)752-9639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ,A.C.C. and Sanchez,D.O. Gene discovery through expressed sequence tag sequencing
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Verdun, R.E., Di Paolo, N.C., Urmenyi, T.P., Rondinelli, E., Frasch
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                                                                                                         Unpublished (1998)
                                                                                                                          Gonzalez Rey,E., Remisz,E., Delgado Garcia,A. and Gonzalez,A. Characterization of ESTs from Trypanosoma cruzi epimastigotes
                                                                                                                                                                                                                                                                         EST
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                                                                                                                                                                                                                                                                                                                cruzi cDNA clone n442.r
AI667900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: dsanchez@inti.gov.ar
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Av. Gral Pa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Instituto de Investigaciones Biotecnologicas (Univ. Nac. de Gral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Sanchez D.O.
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                                                                                                                                                                                                                                 Trypanosoma cruzi
                                                                                                                                                                Trypanosoma; Schizotrypanum (bases 1 to 313)
                                                                                                                                                                                                           Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="T. cruzi epimastigote normalized cDNA Library"
/cell_type="epimastigote"
/note="cDNA Library constructed with oligo dT primed epimastigote mRNA and cloned in pt7t318D phagemid with modified polylinker (PHARMACIA)"

79 c 72 g 46 t 4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="Cl-Brenner"
/db_xref="taxon:5693"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Trypanosoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.9%;
73.7%;
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Pred. No.
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96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 aagcttgcggccgatcaggccgaatatgcggccgcatt 43
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Fax: 34 958 203323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hehl, A., Manger, I., Marra, M., Sibley, L.D., Ajioka, Dietrich, N., Dubuque, T., Hillier, L., Kucaba, T., Waterston, R.H. and Boothroyd, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Toxoplasma gondii
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
                                                                                                                                                                                                                                                                                        High quality sequence stop: 313.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                    relating to organism, clone or library Seq primer: T3
                                                                                                                                                                                                                                                                                                                                                                                Email: toxo@watson.wustl.edu
David Sibley at toxoest@borcim.wustl.edu for further
                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1996)
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1 (bases 1 to 373)
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                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Marra M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WashU-Merck-Stanford-NIH Toxoplasma EST project
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/cell_type="epimastigote"
/note="Site_1: EcoRI; Site_2: NotI; cDNA library
constructed with oligo dt primed epimastigote mRNA and
cloned in pt7t318D phagemid with modified polylinker"
a 91 c 83 g 67 t
Toxoplasma RH Strain tachyzoites were grown in human foreskin fibroblast cultures in vitro. The library was constructed by K.L. Wan, Cambridge University. cDNAs were synthesized from polyA RNAs by oligo d(T) priming and directionally cloned into the EcoRI to XhoI sites of the
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/db_xref="taxon:5693"
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                                                                                                            /Clone="tgzy89b07.r1"
/Clone=lib="TgRH Tachyzoite cDNA"
/Clone_lib="TgRH Tachyzoite cDNA"
/lab_host="XL1-Blue MRF'"
/note="Vector: Lambda ZAP; Site_1: EcoRI; Site_2: XhoI;
                                                                                                                                                                                                       /strain="RH"
/db_xref="taxon:5811"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Trypanosoma"
                                                                                                                                                                                                                                                /organism="Toxoplasma gondii"
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73.78;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brenner"
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97;
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                                                                                                                                                                                                                                                                                                                                                                availability
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aba,T., Wan,K.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (mammalian homologue)
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C. Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schur,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R., and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AW185272 395 bp mRNA EST 19-NOV-1999 se89c06.yl Gm-c1023 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1023-1859 5' similar to TR:P93194 P93194 RECEPTOR-LIKE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabaceae; Papillonoideae; Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vector to vector length is 396.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             info@genomesystems.com web site: www.genomesystems.com
Putative full length read
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Public Soybean EST Project
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314 286 1810
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                                                                                                  DNA was synthesized from mRNA using a poly (dT) sequence with a Not I restrictions site. Sal I linkers adapers were ligated to the blunt-ended cDNA fragments followed by
                                                                                                                                                                               cDNA library was constructed from mRNA isolated from seed coats (100-200mgs) of greenhouse grown plants. The library was prepared using the Life Technologies psuperScript cDNA library construction kit. Complimentary
Not I digestion. The cDNA fragments were directionally cloned into the Not I-Sal I restriction site of the pSPORTI vector. The ligated cDNA fragments were transformed into E.coli Electromax DH10B host cells. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lambda ZapII vector using the ZAP-cDNA synthesis kit (Stratagene). WARNING: the library contains a small percentage of cDNAs derived from the human host cells." 88 c 110 g 109 t 9 others
                                                                                                                                                                                                                                                                                                                                                                             /clone="GENOME SYSTEMS CLONE ID: Gm-c1023-1859"
/clone_lib="Gm-c1023"
                                                                                                                                                                                                                                                                                             /note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; This
                                                                                                                                                                                                                                                                                                                                            /tissue_type="seed coats of greenhouse grown plants"
                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:3847"
                                                                                                                                                                                                                                                                                                                         /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Glycine max"
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                                                                                                                                                                                     Complimentary
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RESULT 13
AV624476/c
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                                                                                                                                                                                                                                                                 agcttgcggccgatcaggccgaatatgcggccg
                                                                                                                                                                                                                                             AGCTGGCGCCCATCATGCGGAATGTGCGGCCG 402
                                                                            MgA0062r MgA Library Mycosphaerella graminicola cDNA clone MgA0062 3' similar to OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM ISOZYME 2, mRNA sequence.
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AV624476 Chlamydomonas reinhardtii 5% to 0.04% CO2 Chlamydomonas reinhardtii cDNA clone LC078c03_r 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Res. (2000) In press
Contact: Erika Asamizu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Asamizu,E., Miura,K., Kucho,K., Inoue,Y., Fukuzawa,H., Ohyama,K.
Nakamura,Y. and Tabata,S.
Generation of Expressed Sequence Tags from low-CO2 and high-CO2
adapted cells of Chlamydomonas reinhardtii
Mycosphaerella graminicola.
                                           AW181098.1 GI:6448332
                                                                                                                                            AW181098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlamydomonas reinhardtii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chlamydomonadaceae; Chlamydomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 48.4%;
Similarity 70.7%;
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Khanna."
a 71 c 82 g 120 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                         dioxide concentration in the bubbling gas was 5% to 0.04\%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Chlamydomonas reinhardtii 5% to 0.04% CO2" /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoI; The cDNA library was constructed from cells cultured
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in a carbon stress acclimatized condition in which carbon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="LC078c03_r"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="C9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Chlamydomonas reinhardtii"
                                                                                                                                                                                                                                                                                                                                       48.4%;
                                                                                                                                            610 bp
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                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                         Score 21.8; DB 37
Pred. No. 1.2e+02;
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Pred. No. 1.2e+02
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REFERENCE
AUTHORS
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AQ399560
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VERSION
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                                                                                                                                         Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, Cler
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQ399560 615 bp DNA GSS 06-MAR-1999 mgxb0014023f CUGI Rice Blast BAC Library Pyricularia grisea genomic clone mgxb0014023f, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cell Biology Department IACR-Long Ashton Research Station Long Ashton, Bristol, BS41 9AF, UK Tel: +44(0)1275 392181 Fax: +44(0)1275 392181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycosphaerellaceae; Mycosphaerella.

1 (bases 1 to 610)

Keon, J.P.R., Bailey, A.M. and Hargreaves, J.A.

A group of expressed cDNA sequences from the wheat fungal leaf
blotch pathogen, Mycosphaerella graminicola
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pyricularia grisea
Eukaryota; Fungi; Ascomycota; Ascomycota incertae sedis;
Magnaporthaceae; anamorphic Magnaporthaceae; Pyricularia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
Contact: Hargreaves JA
                                                                                                     High quality sequence start: 40 High quality sequence stop: 464.
                                                                                                                                                                                                                                                                                                                   Contact: Dean RA
                                                                                                                                                                                                                                                                                                                                    Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                            Genome
                                                                                                                                                                                                                                                                                                                                                                             A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
                                                                                                                                                                                                                                                                                                                                                                                            Yu,Y., Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R., Phillips,K., Sasinowski,M, Wing,R.A. and Dean,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQ399560
AQ399560.1 GI:4370587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: john.hargreaves@bbsrc.ac.uk
Insert Length: 2200 Std Error: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Ascomycota incertae sedis;
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/note="Vector: pSpORT1; Library constructed from cultures
utilizing ammonium ions as a source of nitrogen"
169 c 156 g 159 t 1 others
/organism="Pyricularia grisea"
/strain="70-15"
/db_xref="taxon:89476"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mycosphaerella graminicola"
/strain="Strit"
/db_xref="taxon:54734"
/clone="MgA0062"
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78.8%;
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pred. No. 1.2e+02;
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Search completed: March Job time: 7054 sec
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Best Local Similarity
                                                                                                                   36 AATGCCAGCTTGGAGCCGCTCAAGGCGAAAATGGGCCAGGA 76
                                                                                                                                          1 aatccaagcttgcggccgatcaggccgaatatgcggccgca 41
                                                                                                                                                                                                                 29;
                                                                                                                                                                                                                                                                                                                                                           160
                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                  /clone="mgxb0014023f"
/clone_lib="CUGI Rice Blast BAC Library"
/tissue_type="Protoplasts"
/lab_bost="E. coli DH108"
/note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;
Rice blast is one of the most devestating fungal diseases of rice world wide. It is a filamentous ascomycete with a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25x genome coverage. High density colony filters are available upon request."
50 a 149 c 154 g 151 t 1 others
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                        4,
                                                                                                                                                                                                                                     48.48;
                      2001, 11:46:04
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Pred. No. 1.2e+02;
0; Mismatches 12
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Gapop 10.0 , Gapext 1.0
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45
1 aatccaagcttgcggccgat.....gaatatgcggccgcattat 45
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

C 21	20	19	c 18	c 17		15	14	13	12	11	10	9	8	7	c 6	G	4	Ω	c 2	1	NO.	Result
21.0	21.6	21.8	21.8	22	22	22	22.2	22.2	22.2	22.2	22.2	22.2	23		23.2	23.2	23.2	23.4	23.6	24.8	Score	ı
48.0	48.0	48.4	48.4	48.9	48.9	48.9	49.3				49.3	49.3	51.1	51.6	51.6	51.6	51.6	52.0	52.4	55.1	Match	Query
975611	47811	25458	11627	326301	66441	11936	213190	18622	10121	2565	2565	2013	10908	308373	218971	14724	6254	177241	210047	86896	Match Length	
54	59	29	Н	N	32	1	N	ш	Н	2	ш	2	ш	30	56	58	32	52	56	Ν	DB	
AC007468	AC017664	SCE22	AE004582	NMA6Z2491	PFMAL1P4	AE004219	BSUB0004	AF012532	AE001932	RRAJ2069	AF030293	BACCOTJABC	AE002294	AE003495	AC011697	AC015103	DMU13637	HS402G11	AC010906	RCU57682	ID	
AC007468 Drosophil	AC017664 Drosophil	AL355832 Streptomy	AE004582 Pseudomon	AL162757 Neisseria	AL031747 Plasmodiu	AE004219 Vibrio ch	Z99107 Bacillus su	AF012532 Bacillus	AE001932 Deinococc	AJ002069 Rathayiba	AF030293 Rathayiba	L38014 Bacillus su	AE002294 Chlamydia	AE003495 Drosophil	AC011697 Drosophil	AC015103 Drosophil	U13637 Drosophila	AL022328 Human DNA	AC010906 Homo sapi	U57682 Rhodobacter	Description	

Louis

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REFERENCE
AUTHORS
TITLE
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SOURCE
ORGANISM
                       RESULT 2
AC010906/c
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AUTHORS
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                                                                                                                                              Local Similarity
                                                                           Rhodobacter capsulatus
U57682
U57682.1 GI:1613791
                                                                                                                                                                                                                                                                                          Submitted (07-MAY-1996) M. Fonstein, MGCB, Univ 58th, Chicago, IL 60637, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                    Kumar, V., Fonstein, M. and Haselkorn, R. Bacterium genome sequence Nature 381 (6584), 653-654 (1996)
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Homo sapiens chromosome
                                                                                                                                                                                                                                                                                                                                      Direct Submission
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46.7 10186
46.7 11266
46.7 11266
46.7 151802
                                                                                                                                  Conservative
                                                                                                                                                                                                           /organism="Rhodobacter capsulatus"
/strain="SB103"
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/db_xref="ftaxon:1061"
/map="cosmids 143-147 of the complete encyclopedia"
/map="cosmids 143-147 of the complete encyclopedia"
            210047 bp
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                                                                                                                                              55.1%;
80.6%;
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7 AC047083
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7 G23787
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AC007503
AL354867
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                                                                                                                                              Score 24.8;
Pred. No. 48;
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2 clone RP11-56604, WORKING DRAFT SEQUENCE,
                                                                                                                                   Mismatches
                                                                                                                                                           DB 2; Length 86896;
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L29299 Frankia aln
M17788 M.luteus st
AE005138 Halobacte
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              20-AUG-2000
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  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chemistry: Dye-primer ET; 69% of reads Chemistry: Dye-terminator Big Dye; 31% of reads assembly program: Phrap; version 0.990319 Consensus quality: 197418 bases at least Q40 Consensus quality: 202189 bases at least Q30 Consensus quality: 204884 bases at least Q30 Consensus quality: 204884 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 210047)
                                                                                                                                                                                                                                                                                                                                                                                                     * NOTE: This is a 'working draft' sequence. It currently * consists of 12 contigs. The true order of the pieces * is not known and their order in this sequence record is * is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insert size: 203000; agarose-fp
Insert size: 208947; sum-of-contigs
Quality coverage: 4.78 in Q20 bases; agarose-fp
Quality coverage: 4.63 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing vector: M13; 85%
Sequencing vector: plasmid; 15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: H_NH0566004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MO 63108, USA on Aug 13, 2000 this sequence version replaced gi:9211497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (25-SEP-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 210047)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                               * arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown
* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site:http://genome.wustl.edu/gsc/index.shtml
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                                                                                                                                                                                                                                                                                                                                    as soon as it is available and the accession number will be preserved.
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73430
73530
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6000
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12340
12440
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20569
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    Location/Qualifiers
1. .210047
                            119615: gap of unknown length
154482: contig of 34867 bp in
154582: gap of unknown length
210047: contig of 55465 bp in
                                                      119615: gap of 154482: contig
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1669: gap of
5999: contig
6099: gap of
12339: contig
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94751
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g of 14549 bp in
f unknown length
g of 14575 bp in
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of 4330
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of 8029
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of 6240 bp in length
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                                                                                                                                                                                                                                                                                                                            Human DNA sequence from Clone RP3-402G11 on chromosome 2G13-31-13.33 Contains the MAPK12 gene for mitogen activated protein kinase 12 (SAPK3), the MAPK11 gene for mitogen activated protein kinase 11 (PRKM11), gene KIAM315, the gene for a novel protein similar to KIAM30901 and mouse histone deacetylase MHDA2, the gene for a novel protein similar to Kenopus gamma-tubulin interacting protein (yeast SP98 homolog), the gene for a novel protein similar to C. elegans F38A5.2, the gene for a novel protein similar to C. elegans F38A5.2, the gene for a novel protein similar to MRS1 and the gene for a novel protein similar to MRS1 and the gene for a novel protein similar to mouse MOV10 (GB110) and yeast and plant predicted proteins. Contains ESTS, GSSs and fifteen putative CpG islands,
Submitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                AL022328.21 GI:5263010
HTG; CpG island; GB110; KIAA0315; KIAA0901; kinase; MAPK11; MAPK12;
MHDA2; mitogen_activated_protein kinase; mitogen-activated; MOV10;
                                                                                                            Eukaryota: Metazoa: Chordata: Craniata; Vertebrata: Euteleostomi; Mammalia: Eutheria: Primates: Catarrhini; Hominidae: Homo
                                                                           Coville, G
                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                        complete sequence.
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                                                                                                                                                                                                         PRKM11; SAPK3; SPC98
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50410 c 48661 g 53321 t
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154583. .210047
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1670. .5999
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/db_xref="taxon:9606"
/chromosome="2"
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76.3%;
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Pred. No. 1.1e+02;
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/note="L2 3959. .445

repeat: matches 2630.

.2643 of consensus"

.527 of consensus"

.308 of consensus .303 of consensus" .3086

'note="AluSp repeat: matches 1. .300 of consensus"

2663.

/note="AluSq repeat: matches 1. .306 of consensus" 2504. .2574

/note="AluSx repeat: matches 1.

.298 of consensus"

.1659

note="AluSg repeat: matches 1. .310 of consensus"

/note="MER58 repeat: matches 170. .243 of consensus"

12 repeat: matches 2643. .2747 of consensus"

/note="MER1A repeat: matches 31.
5044. .5270

6305.

note="match: GSS: Em:AQ475194" /note="AluJo repeat: matches 29. /note="AluJb repeat: matches 77.

/note="AluSx repeat: matches 1. .294 of consensus"
9427. .9542

/note="AluYb8 repeat: matches 1. .318 of consensus 'note="AluY repeat: matches 1. .303 of consensus"

/note="AluY repeat: matches 1. .303 of consensus" note="AluJo repeat: matches 30. .150 of consensus" ş

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Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence is the entire insert of clone RP3-402G11 The true right end of clone RP5-898I4 is at 23403 in this sequence. The tright end of clone RP1-332E17 is at 56734 in this sequence. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP3-402G11 is from the library RPCI-3 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                requests: clonerequest@sanger.ac.uk
on Jun 29, 1999 this sequence version replaced gi:5262835.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        During sequence assembly data is compared from overlapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VECTOR: pCYPAC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr22
                                                                                                                                                                                                                                                                                                                                                                                                                                     right end of clone RP4-600024 is at 96013 in this sequence.
/note=";
657..9
                                                                                                                                                                                               /map="q13.31-13.33"
                                                                                                                                                                                                                                              /chromosome="22"
                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                  /clone_lib="RPCI-3"
                                                                                                                                                             /clone="RP3-402G11"
                                  AluSx repeat: matches 1. .312 of consensus'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="AluY repeat: matches 2.
15488. .15718
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22246. .22887
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/note="AluY repeat:
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11642. .11957
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10804. .11101
/note="Aluy repeat: matches 1.
31363. 31990
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21958._22115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="MER46C repeat: matches 113. .337 of consensus"
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                                        /note="LIMC/D repeat: matches 5325. .5397 of consensus"
31048. .31362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="L1 repeat: matches 2915. .3769 of consensus" 24501. .24747
/note="L1MEC repeat: matches 1501. .1751 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="FRAM repeat: matches 1. .166 of consensus"
23152. .23217
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28694. .28997
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23699. .24482
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                                                                                    30975
                                                                                                 /note="L2 repeat: matches 1079. .1303 of consensus"
                                                                                                                          30567
                                                                                                                                                                                 /note="Alusx repeat: matches 24. .304 of consensus"
                                                                                                                                                                                                                            /note="L1ME repeat: matches 5189. ,5489 of consensus"
                                                                                                                                                                                                                                                                  /note="AluJo/FLAM repeat: matches 3. .133 of consensus"
                                                                                                                                                                                                                                                                                                        /note="Alusg repeat: matches 1. .304 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="L1 repeat: matches 3780. .3926 of consensus"
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                                                                                                                                             /note="L1ME repeat: matches 5086.
                                                                                                                                                                                                                                                                                                                                                                                                                              'note="L1MEc repeat: matches 272. .492 of consensus"
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23373
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                           .303 of consensus"
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                                                                                                                                               consensus"
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RESULT
DMU13637
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                  The Drosophila yolkless gene encodes a vitellogenin receptor belonging to the low density lipoprotein receptor superfamily proc. Natl. Acad. Sci. U.S.A. 92 (5), 1485-1489 (1995)
                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 6254) Schonbaum, C.P., Lee, S. and Mahowald, A.P.
                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                              Genetics and Cell Biology, The University Street, Chicago, IL 60637, USA
                                                                                                                                                                                                                                  Submitted (15-AUG-1994) Christopher P. Schonbaum, Molecular Genetics and Cell Biology, The University of Chicago, 920 E
                                                                                                                                                                                                                                                                 Schonbaum, C.P.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fruit fly
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/note="LIMC/D repeat: matches 3936. .4184 of consensus"
33468. .33637
/note="FRAM repeat: matches 1. .175 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="L1MC/D repeat: matches 4184. .4755 of consensus"
32908. .33208
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/tissue_type="ovary"
/dev_stage="adult"
145. .6099
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/note="Alusg repeat: matches 1. .310 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="L1MEc repeat: matches 2231. .2385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="AluSx repeat: matches 1. .288 of consensus"
                                                                                                                                                                                               Location/Qualifiers
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                                                                       /chromosome="1"
                                                                                      /map="12E4-12E8; 1-48
                                                                                                        /clone_lib="gt11 ovary cDNA library of al., Mol. Cell Biol. 9:5726(1989)"
                                                                                                                                          /db_xref="taxon:7227"
                                                                                                                                                          /organism="Drosophila melanogaster'
                                                     /sex="female"
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73.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 23.4; DB 52;
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vitellogenin receptor (yl) mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   matches 1. .297 of consensus'
                                                                                             CM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-MAR-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                Steinhauer
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ORIGIN
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                                                                                                                                                                                                                                               polyA_site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           variation
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                                                                                              Local
2 atccaagcttgcggccgatcaggccgaatatgcggccgcattat 45
                                                                                           Similarity
                                                                                                                                                                                                     1394 a
                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="FlyBase:FBgn0004649"
/replace="c"
6254
                                                                                                                                                                                              /note="6 A residues"
1677 c 1910 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KGFRLAKFEDKCEDVDECKEQDDLCSQGCENTSGGYRCVCDAGYLLDKDNRTCRAVVY
GSKEQOPLLLYTTOMTIMGMHLREDNVRNHVYQVAGNLSKVIGVAYDGSHIYWTNIQN
EAESIVKANGDGSNAEILLTGGLAFPEDLAVPMLTQNIYFSDNIMRHIAVCSNOGLNC
AVLVTQDVHQPRSLAVPPQKGLMFWDDGEKPMIGRASMDGSBRSRPIYSDNIEWPHGL
ALDMHQQRIYWVDAKLGSVQTVRPDGTGRRTVLDGMLKHPYGLAIFEDQLYWSDWATK
SVHACHKFSGKDHRILAKDRTIYAVHIYHPAKQPNSPHGCENATCSHLCLLABPEIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLGGTKAFLEHERAEAGVGFTTETGTVSSRGSNDTFTTTSASSSFAAQQFSVPNALQR
LLRPRQSASGDPMAQELLLESPSRESKLHALDGGGAGGDGDGGCGVGRQVPDILVADM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQEIQACSFVGRMCGRIVHVKSPRHYKHLAVDGYHARIFYIVIRTEGYGQTSSEIHMA
RLDGSRRDMLLQRSESFMTALITDPHQQLLYFVDQHMRTLERISYRLKTGPMRRPEIM
LQKSNALMHPSGLSYYENNAFIVNLGSMEAVQCALYGSRICHKISINVLNAQDIVVAG
RSRQPQKASHPCAHAHCHGLCLQADYGYECMGNRLVAEGERCPHGSGNEVAVLGAVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDDAAKSAGQFGGNYAGNDANARFVS."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLELEHEHEQNGHFHWLMALFVLAAGSLIAGLGYMYYQYRQRGHTDLNINMHFQNPLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSCACPDGMRLAPDHRRCMLMEKRQRLFIGLGQVLLEIBHTAFGAHQVSKSYTLPCLI
NEMVVNRINGSLIADNDQRLILEFQPESHESNVLVRSNLGNVSALAFDHLSRNLYWA
DTERAVIEVLSLQTRHRALIRFFFGQEVPIGLTVMPABGYLYVVLKAKHSHIDKIPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TSSRYGNOORTHLIINGRHVAISLLLLLVGLCGGTAAGTPGSADTRCDAGOFQCRDGGC
ILQAKMCDGRGDCKDSSDELDCDYRLCRPPHWFPCAQPHGACLAAELMCNGIDNCPGG
EDELNCPVRPGFRFGDTAHRMRSCSKYEFMCQQDRTCIPIDFWDGRPDCTDKSDEVA
                                                                                                                                                                                                                                                                                                                                /gene="yl"
                                                                                                                                                                                                                                                                                                                                                                        /db_xref="flyBase:FBgn0004649"
/replace="g"
                                                                                                                                                                                                                                                                                                                                                                                                              /note="iso-1 (genomic DNA)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="FlyBase:FBgn0004649"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NRETCLTLSEVCDGHSDCSDGSDETDLCHSKPDCDAKKCALGAKCHMMPASGAECFCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCKQAEITCPGEGHLCANGRCLRRKQWVCDGVDDCGDGSDERGCLNLCEPQKGKFLCR
                                                                                                                                                                                                                                                                                                            'note="iso-1 (genomic DNA)"
                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="yl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               replace="a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="iso-1 (genomic DNA)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'gene="yl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="MCQAEHQVHPSEQRIRVESPKMTASRRGFNLTSQTRAHPSSGGS/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAB60217.1"
/db_xref="GI:535346"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="putative vitellogenin receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /standard_name="yolkless"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               db_xref="FlyBase:FBgn0004649"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /allele="
                                                                                           51.6%;
70.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            olkless"
                                                                       0;
                                                                                       Score 23.2; DB 3: Pred. No. 2.6e+02.
                                                                   Mismatches
                                                                                                         DB 32;
                                                                     13;
                                                                                                           Length 6254;
                                                                0;
                                                                Gaps
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JOURNAL
REFERENCE
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AC011697/c
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
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AC015103
LOCUS
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                                                          AUTHORS
                                                                                                                            TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8691 ATCCAAGCGTGCAGTTTCGTGGGACGCATGTGCGGCCGCATTGT 8734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4810 ATCCAAGCGTGCAGTTTCGTGGGACGCATGTGCGGCCGCATTGT 4853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 atccaagcttgcggccgatcaggccgaatatgcggccgcattat 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31;
2 (bases 1 to 218971)
Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blaze Butenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L., Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.I.
                                                                                                                                    Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hinkle, A., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Lee, B., Lewis, S., Li, P., Ling, H., Moshrefi, A.R., Moshrefi, N., Nixon, K., Pacleb, J.M., Pacleb, J.M., Pacleb, J.M., Pan, K.H., Webster, D., Wicklas, S., Sethi, H., Svirskas, R.R., Wan, K.H., Webster, D., Weolley, P., Yang, S., Ye, M., Yu, C. and Rubin, G.M.
                                                                             Unpublished 2 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC011697 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster chromosome X clone BACR12J05 (D884) RI 12.J.5 map 12E-12E strain y; cn bw sp, *** SEQUENCING IN PROGRESS, 125 unordered nieres
                                                                                                                   Sequencing of Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC011697.7 GI:6978356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 14724)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence was identified as CDM: 10209883 by the submitter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adams, M. and Venter, J.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HTG; HTGS_PHASE2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fruit fly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC015103.1 GI:6436232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or further information on this sequence e-
NOTE: This is a 'working draft' sequence.
This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the accession number will be preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      by the finished sequence as soon as it is available and
                                                                                                                                                                                                                                                                                                                           (bases 1 to 218971)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218971 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.6%;
70.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 23.2; DB 51
Pred. No. 2.3e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence e-mail to fly@celera.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IN PROGRESS ***, in ordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 14724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-NOV-1999
                                               Blazej, R.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (D884) RPCI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RPCI-98
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COMMENT
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On Feb 15, 2000 this sequence version replaced gi:6838484.
On Feb 15, 2000 this sequence version replaced gi:6838484.
For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgpefruitfly.berkeley.edu. All contigs in this submission meet the following cutoffs: length >= 200 bases.

* NOTE: This is a 'working draft' sequence. It currently consists of 125 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are unknown.

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence will
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       Adams, M.D., Celniker, S.E., Holt, R.A., Evans, C.A., Gocayne, J.D., Adams, M.D., Celniker, S.E., Li, P.W., Hoskins, R.A., Galle, R.F., George, R.A., Lewis, S.E., Richards, S., Ashburner, M., Henderson, S.N., Sutton, G.G., Wortman, J.R., Yandell, M.D., Zhang, Q.C., Chen, L.X., Sutton, G.G., Wortman, J.R., Yandell, M.D., Zhang, Q.C., Chen, L.X., Barandon, R.C., Rogers, Y.H., Blazej, R.G., Champe, M., Pfeiffer, B.D., Wan, K.H., Doyle, C., Baxter, E.G., Helt, G., Nelson, C.R., Gabor Miklos, G.L., Abril, J.F., Agbayani, A., An, H.J., And, H.J., Andrews-Pfannkoch, C., Baldwin, D., Ballew, R.M., Basu, A., Andrews-Pfannkoch, C., Baldwin, D., Ballew, R.M., Beeson, K.Y., Baxendale, J., Bayraktaroglu, L., Beasley, E.M., Beeson, K.Y., Benos, P.V., Berman, B.P., Bhandari, D., Bolshakov, S., Borkova, D., Botchan, M.R., Bouck, J., Brokstein, P., Brottier, P., Burtis, K.C., Busam, D.A., Butler, H., Cadleu, E., Center, A., Chandra, I., Cherry, J.M., Cawley, S., Dahlke, C., Davenport, L.B., Davies, P., de Pablos, B., Delcher, A., Deng, Z., Mays, A.D., Dew, I., Dietz, S.M., Dodson, K., Doup, L.E., Downes, M., Dugan, Rocha, S., Dunkov, B.C., Dunn, P., Durbin, K.J., Evangelista, C.C., Ferraz, C., Ferriera, S., Fleischmann, W., Fosler, C., Gabrielian, A.E., Garg, N. S., Gelbart, W.M., Glasser, K., Glodek, A., Gong, F., Gorrell, J.H., Gu, Z., Gan, P., Harris, M., Harris, M.L., Harvey, D., Heiman, T.J., Wei, M.H., Ibegwam, C., Jalali, M., Kalush, F., Karpen, G.H., Ke, Z., Kennison. J.A., Ketchum, K.A., Kinmel, H.B.E., Kodira, C.D., Kraft, C.,
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181860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .82861
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183108:
183760:
183760:
183840:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180521:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      d: contig or all the contig or all the contig of 497 bp in 1,285: gap of unknown length 9653: contig of 1368 bp in length 9653: contig of 788 bp in length 9658 bp in length 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gap of contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gap of
contig
gap of
contig
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contig of 248 bp in length
gap of unknown length
contig of 572 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gap of unknown length
contig of 516 bp in length
gap of unknown length
contig of 841 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gap of unknown length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown length
of 624 bp in length
unknown length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown length of 511 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       No. 1.6e+02
Kimmel, B.E., Kodira, C.D., Kraft, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 218971;
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RESULT

FOCUS

VERSION

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MEDLINE
REFERENCE
AUTHORS
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
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Li,J., Li,Z., Liang,Y., Lin,X., Mattei,B., McIntosh,T.C.,
McLeod,M.P., McPherson,D., Merkulov,G., Milshina,N.V., Mobarry,C.,
Morris,J., Moshrefi,A., Mount,S.M., Moy,M., Murphy,B., Murphy,L.,
Muzny,D.M., Nelson,D.L., Nelson,D.R., Nelson,K.A., Nixon,K.,
Nusskern,D.R., Pacleb,J.M., Palazzolo,M., Pittman,G.S., Pan,S.,
Pollard,J., Puri,V., Reese,M.G., Reinert,K., Remington,K.,
Sunders,R.D., Scheeler,F., Shen,H., Shue,B.C., Siden-Kiamos,I.,
Simpson,M., Skupski,M.P., Smith,T., Spier,E., Spradling,A.C.,
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Venter,E., Wang,A.H., Wang,X., Wang,Z.Y., Wassarman,D.A.,
Worley,K.C., Wu,D., Yang,S., Yao,Q.A., Ye,J., Yeh,R.F.,
Zaveri,J.S., Zhan,M., Zhang,G., Zhao,Q., Zheng,L., Zheng,X.H.,
Zhong,R.A., Myers,E.W., Rubin,G.M. and Venter,J.C.
The genome sequence of Drosophila melanogaster
NF 20146606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            On Oct 9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rockville, MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adams, M.D., Celniker, S.E., Gibbs, R.A., Rubin, G.M. and Venter, C.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20196006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000 this sequence version replaced gi:7292953.
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GGHG I GPVPSAYPNGGAFPAGPTNGGAFAGGPTNAAFQLPPGGPFGPQAGNFAQPGGE

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gene
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                                                     gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PQAGGFPPQGAGFQPQGIPGNGFPTQGAPFSPQQGVFPSQGGAFGPQGIPGNGFLGGN
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                                                                                                                                                    .16455,16506. .>17307)
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AE002294
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REFERENCE
AUTHORS
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ORGANISM
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ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AE002294 10908 bp
Chlamydia muridarum,
AE002294 AE002160
AE002294.1 GI:71903
                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 10908)

Read, T.D., Brunham, R., Shen, C., Gill, S.R., Heidelberg, J.F., White, O., Hickey, E.K., Peterson, J., Umayam, L.A., Utterback, T., Werry, K., Bass, S., Linher, K., Weidman, J., Khouri, H., Craven, B., Bowman, C., Dodson, R., Gwinn, M., Nelson, W., DeBoy, R., Kolonay, J., McClarty, G., Salzberg, S.L., Eisen, J. and Fraser, C.M.

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlamydia muridarum Chlamydia muridarum
                                                                                                                                                                                                                                                                         Submitted (01-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic Acids Res. 28 (6), 1397-1406 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pneumoniae AR39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10684935
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SHGSYSGSSGSGHGYGSGSSHGSGVRSGHGSSFGSGHKSGSYAANGGYEYRLKH"
complement(join(<17993. .18361,18516. .>18623))
/gene="CG13403"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MPAGPTPYSSGGSSYAAPSVSHYSYSAPAASASASHVSYSAPAA
AHSSYAAPSVSHGSYSAAFVAAPSRYXLAPAAVSHSSYSAPVVSRKSYSAP
AVSHGSYSSGGSGGSGAFAVASYSSYSAPAASHTSYSAPVAAPSROYLAPAASSYSA
PAVSSYSAPAVSSYSAPAVSSYSAPAVSHGSSYSTSSLSHGSYAAPSVSSKTYAAPAPAV
                       /note="hypothetical protein; identified by Glimmer2;
putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="FLYBASE:FBgn0030543"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                 /organism="Chlamydia muridarum"
/db_xref="taxon:83560"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="FLYBASE:FBgn0030544"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="CT32756"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="GI:7292958"
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                                                             /gene="TC0265"
                                                                                                             /gene=
                                                                                                                                                          /note="synonym: Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               muridarum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="FLYBASE:FBan0013403"
                                                                                                                                                                                                                                                 .ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chlamydiales; Chlamydiaceae; Chlamydia
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/codon_start=1
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70.5%;
                                                                                                               C0265"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16455,16506. .17307)
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                                                                                                                                                              MoPn"
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                                                                                                                                                                                                                                                           /translation="meyflgweymgikgyggsghsdydipshngdgeseknssdstss
Kynakytsslogapstudensyspysyddyddliesgessrhyikksieteeaahres
syegachssrciegklogligklarrygeavrntygsifpakabeortgkartnysp
sasrglrlmetdewryrylhrnypmoclfakldadeaedmaaytkeyysplekegab
retieelcomyaknwekrardledmgaakkfludpeggsdpkykgtlogytygntmey
                                                                                                                                                                     DGPGVSKLSEVDTGFWLDMEKLSDAVLSANIOKGLRARRVLNOSIPQLESLEERRRKL
ESACDEARASLKEAGWIKEGKEPNKAQRAFRRFVEESRNLELSFGSFGESARRLSARV
SQGLAAAGEAIRRCFDCRKGKYSLKKOLSSEELNLAEELIRFTDEMGIERDPDGNYNI
complement(5923. .6192)
                                                            complement(5923. .6192)
                                                                                      MRNYIVSQPQEQIPNSEQVEQLFQELINDGDQIIQELMKIWNEELDNQ'
                                                                                                               PWVENWRTGVPVIEGEGAEHIYETMMPVQESFEQVYEVMDMGLEERRDFAVSQOHYQV
PPRSSLNYETPRFREYDVPRNSARSYYDVPRVPPQNEVEEMHVTKGMRSSVYACFVAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3956
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SLPKGLPHPDLPDGNLSSHFGYQGDWNFSWQTSDQRETLVANWTANSYIPHPERQSAL
VANTLWNTYSDMQAVQSMINTTAQGGAYLFGTWGSAVSNLFYSHGNSGKSTDNWKHRS
LGYLFGISTHSLDDHSFCLAAGQLFGKSSDSFYTSADTTSYIAAIQTQIATSLIKISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LRHNGPVSFVNNSAKLGGATATQSGGSLSTTAGGGSVLFQNNSCHESDQGTVRNATYL
EKNALLSSLEARHGDILFFDPTVQEVVSPEFSTTSALTPLRIQTNTNRAVIFSSENLS
KEEKTEANLISKIQQPIELQSGCLVLKDRVILSAPSLSQAPQALLVMDYGTSLTTSSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRFLSFTDCSSSTEDSPSILYHKNGQLFLRNNGNMSFYRNHSEGSGGALSTDALFLQH
NYLFTNFEENSSAKNGGAIQAQTLSLSRNYSSLSFSRNRANLNGGAICCQNLICSGNV
NPLFFTNNSALNGGAICCINEQNLSEKGCLSLAYNQETLFSGNSAKEKGGAIYTKHMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="polymorphic membrane protein G family"
/protein_id="AAF39136.1"
/db_xref="01:719308"
/translation="MRPDHVNLCCLCATILSPTAILFGQDALDKSALITKNPNSIVCTFLEDCTMENFSPALLSHARQDDPLYIIGNTHNWFVSNLHPSTNEERFLKEKGDLSIQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="TC0267"
/note="similar to GP:4376270; identified by sequence
similarity; putative"
                                   /gene="TC0269"
                                                                                                                                                                                                                                                                                                                                                                                                                    /transl_table=11
/product="hypothetical protein"
/protein_id="AAF39137.1"
/db_xref="GI:7190309"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    putative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QACYNESIHELKTKYRSFSKEGFGAWHSVAVSGEIGASIPIVSNGSGLFSSFSIFSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(1104. .3707)
/gene="TC0267"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="hypothetical protein"
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FWGHOKSCFLFHKVKVSTWFVPYKVVGFFVQRLLDHLLKK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="hypothetical protein; identified by Glimmer2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RCVESGPVTLLKNSVTWDAPMANLDSRAWMFRLTNQRALHRFQTLVNMSYMLRGQSYS
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HTESAKIYHQNRKRCHKVGCWGKVKRFLCCCCCAEKEWVEGKITGLGLWMQEHIRLHG
ILITGYAVHLSGVCWENMLLAGETLSPGDQRQLNAALENSSITWMRLMLDSSDGKVDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'gene="TC0268"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="hypothetical
/protein_id="aaff39135.1
/db_xref="GI:7190307"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="TC0266"
426. .1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="TC0266"
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.1"
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/note="conserved hypothetical protein; identified by
Glimmer2; putative"
                                                                                                                                                                                                         NGKAKALGFLVGQIMKRTEGKAPPKRVNELLLAAMRDA" complement(9731..10834)
                                                                                                                                                                                                                                                                                                                                                                                  VCTGMPGALPVLNKDAVRKAVLFGCAVEGDVALFSRFDRKSYFYPDSPRNFQITOYEH
PIVRGGCVRAIVEGEEKTFELAQTHLEDDAGMLKHFGDFAGVDYNRAGVPLIEIVSKP
CMFSAEDAVAYANALVSILSYIGISDCNMEEGSVRFDVNISVRPKGSKELRNKVEIKN
                                                                                                                                            complement(9731. .10834)
                                                                                                                                                                                                                                                                                            DYMYFVEPDLPVLQITESYIDEVRQTLPELPHSKYMRYITDFDLAEDLAMILVSDRHT
AHFFETATMSCKNYRALSNWITVEFAGRCKATGKTLPFTGILPEWVAQLVNFIDRGVI
                                                                                                                                                                                                                                                                                                                                                  MNSFTFMAQALEAEKHRQIEEYLSHPNEDPKKVVPAATYRWDPEKKKTVLMRLKERAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="glutamy1-tRNA(Gln) amidotransferase subunit B"
/protein_id="AAF39140.1"
/db_xref="GI:7190312"
/translation="MGIAHTEWESVIGLEVHVELNTASKLFSPARNHFGDEPNTNISP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MQEMYARSRKEGFGKEVTRÄILLGNYVLSAERONIFYKKGTAVRATLIEAFOSAFECC
DVIAMPVCASPAIRDTDVLDPYSLYLQDIYTVAVNLAYLPAISVPSGLSKEGLPLGVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CKERALLRASRIDDKLAKGDPIGILAGIPIGVKDNIHITGVKTTCASKMLENFVAÞFD
ATVVRRIEMEDGILLGKLNMDEFAMGSTTRYSAFQHTNNPWDLERVPGGSSGGSAAAV
SARFCPIALGSDTGGSIRQPAAFCGVVGFKPSYGAVSRYGLVAFGSSLDQIGPITTVV
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6707. .8182
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VAIDISDIILEATVHHFVGPEDLREDMVTSDFTREEFLANVPVSLGGLVKVPTVIK"
6707. .8182
/transl_table=11
                            /codon_start=1
                                                                                                                      /gene="TC0273"
                                                                                                                                                                            /gene="TC0273"
                                                                                                                                                                                                                                                                  PGKIAKETADKMVSSFGESPEDILRRHPSLLPMTDDHALRAIVKEVVAQNAASVEDYK
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6393. .6695
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/transl_table=11
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putative; identified by match to TIGR protein family HMM
TIGR00135"
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Glimmer2; putative"
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TQAAYVVAGIAGVIAFLNFFKCCFKKRHSDCCSSKGGCHHHTDRE"
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/protein_id="aAF39138.1"
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Bacillus subtilis cotJABC operon, polypeptide(s) affecting spore
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SIANTERSLRSEEVLHSQSLLRQKELFPNTSNIKKELPNTKSILHTPLNRRSPSGSDS
DDYYYTPRAGLSSAETSALGDISGISSSSTSSKTSTPKAKRRVVRSSRSERNARHHRN
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PFILTGTAAGLMFSAIAVGGGAVILANPLFLMGSMTLGFALMSLHKVTYQYLSNNSQW
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                                                                                                                                                                                                                                                        /gene="cotJB"
519. .821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Bacillus subtilis"
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            /gene="cotJC"
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THPHDEDALKQFNQYSGYSRHLKRQFESSYGPLLQFGNSPAGKDWDWGKGPWPWQV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1996)
2 (bases 1 to 2565)
Labadie, J.C.
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Submitted (17-OCT-1997) TPA, INRA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cloning and sequencing of a kinase gene from the bacteria Rathayibacter rathayi equivalent to the kdpD gene from Escherichia
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a 426 c 553 g 519 t
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EKWGDVEAILLDAGIDVMSTVNIGHIESLTDVVKKTTGAPQRETIPDEVLRARAEIEV
IDVTPVAAGALASGLVVPAERIDAALSNYFRLGNLTGLRELALLWLAVGADGTAPT
RAGGIDSTWETRERVVVALTGGPEGDSHPPGATHCRPCGRGELLAVHVTGADGTAPFT
RAGGIDSTWETRERVVVALTGGPEGDSHPPGATHCRPCGRGELLAVHVTGADGTAPFT
RAGGRENTUNHIVNHAAAGGRETLPRHAGGALTVKRRLSGLALTLILGPLITAVLV
TFRSPDSITSDVLTYQVLVALVGGIMPALLAAVLSGITLDVFLVEPLFTVTVDKP
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                                                                AVSHDLRRPFDGGNQKGGWLALHRDDPVCRRPGGAARDRRRKPAHLSVLVTDLLDVSR
VQAGVLGVTVRQVDVEDVLPRALDELGVGPDQVVLDLDAAVGPVLADPGLLQRVLVNL
LANALRFSPBGAVPTIDQSFGDTVQIRVTDHGPGIAADRRDDVFVPFQRLGDTDNSTG
                                                                                                                                         LHLFALALYITIAMMVSYVVDQAARRTRVARRSAAESELLATIAGSVLRGDGALQSLV
SRTRKVWVEGCDCWMPRVRPITPTRPPGADGQTAADHAVICADGEPASDDRVVLVPVG
ERATLELHGADLDASERRLLAVIAAQIDAALEHEALSVTAREVGPLAETDRVRTALLS
                                                                                                                                                                                                                                                                                                                                                                                                       /product="protein kinase KdpD"
/protein_id="AAB84261.1"
/db_xref="GI:2613049"
                      LGLGLALSKGFTVGMGGELDTEDTPGGGLTMVVTLPVASADADANADRPGGSRASL" 771 c 931 g 475 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similar to E. coli sensor protein KdpD"
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69.8%;
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Pred. No. 6.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (17-OCT-1997) Labadie J.C., TPA, Theix, 63122 St Genes Champanelle, FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Micrococcineae; Microbacteriaceae; Rathayibacter. 1 (bases 1 to 2565)
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27; Conserv
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                                                                                                                                   Conservative
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AEQGIDSTWETRERVVVALTGGPEGDSHEPGATHCREVGRGELLAVHYTGODEFAPPT
RGLWARQRSLVESLGGSYHQVIGDDIALVEFARAANATQLVGYSRRGRLARRCPYRGS
VDGHRESGNIVHI VNHAAAGGRETLERMAGGALTVKRRLSGLALTLLIGPLTTAVLY
TERSPDSITSDVLTYQVLVVLVALVGGIWPALLAAVLSGITLDYFLVEPLFTYTVDKP
LHLFALAVITIAMMVSYVDDOAARRTVARRSAAESSELAFTLAGSVLRGDGALOSLV
SRTRKVWVEGCOCWHEPKPTTFTREPGADGGTAADHAVICADGEPASDBRVVLVPV
ERSTRSVALTGENALAVIAQIDAALEHEALSVTAREGFLASTLAGSVLRDDALOSLV
SRTRKVWVEGCOCWHEPKPTTFTBADGTOTAADHAVICADGEPASDBRVVLVPV
ERATLELHGADLDASERRLAVIAAQIDAALEHEALSVTAREVGPLASTDRVVZTALLS
AVSHDLRREPGDGOROKGWLALHRDDPVCRREGGAADBRRKVAHLSVLVTDLLDVSR
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771 c 931 g 4.75 t
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EKRWQDVEAILDAGIDVMSTVNIQHIESLTDVVHKITGAPQRETIPDEVLRAAREIEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="protein kinase"
/protein_id="CAA05169.1"
/db_xref="GI:2564305"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="SWISS-PROT:034971"
/translation="MLVGARVLLGAPRGVGKTFTMLEEAKPLRDEGVDVVVAVVETHG
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/strain="2 J"
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77.18;
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Pred. No. 6.6e+02;
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White, O., Elsen, J.A., Heidelberg, J.F., Hickey, E.K., Peterson, J.D., White, O., Elsen, J.A., Gwinn, M.L., Nelson, W.C., Richardson, D.L., Dodson, R.J., Haft, D.H., Gwinn, M.L., Nelson, W.C., Richardson, D.L., Moffat, K.S., Qin, H., Jiang, L., Pamphile, W., Crosby, M., Shen, M., Yamathevan, J.J., Lam, P., McDonald, L., Utterback, T., Zalewski, C., Makarova, K.S., Aravind, L., Daly, M.J., Minton, K.W., Fleischmann, R.D., Ketchum, K.A., Nelson, K.E., Salzberg, S., & Smith, D., Venter, J.C. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    White,O., Elsen,J.A., Heidelberg,J.F., Hickey,E.K., Peterson,J.D. Dodson,R.J., Haft,D.H., Gwinn,M.L., Nelson,W.C., Richardson,D.L., Moffat,K.S., Qin,H., Jiang,L., Pamphile,W., Crosby,M., Shen,M., Vamathevan,J.J., Lam,P., McDonald,L., Utterback,T., Zalewski,C., Makarova,K.S., Aravind,L., Daly,M.J., Fraser,C.M. et,al. Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (08-NOV-1999) The Institute for Medical Center Dr, Rockville, MD 20850, US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       radiodurans R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Deinococcus radiodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Deinococcus radiodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AE001932 AE000513
AE001932.1 GI:64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria;
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                                          */translation="myceinllpkeyrrosopsvwkyaswaagltaavlggwflsvsg
dtnolrersaaloolidavafoksrfnoltagoeelekvtovatrolrdoktywsnula
sfyervpgnvyfsnvmstvapgaseslayagoeelekvtovabltrosarsopalvogflab
etdsnegvdfkgmohdatngiytftasigvvgdopsaapgadptaggapatgtapaap
AAPAPTATTPAAAPAQGGAQ"
2053. .2712
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RLAGLEPTVVDLKSFAALRALRGNLLGEHLTKSTLTGTNYTEAGEVALVMEIGASSSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to
53.56; identified
/codon_start=1
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1340. .2056
                                                                                                                                                                                                                                                                                                                                                                                    GLAAAIGDALGFGVEVASPWLTVQTDQAGVDTGYLQTNAPEFTVPLGLALRGVMGRG'
                                                                                                                                                                                                                                                                                                                                                                                                         NFDLSREQYSPARVFEVVRPVLGDLITEIRRSLEFYRVQSGDVVIDRTFLAGGGAKLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="DR0770"
172. .1347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:1299"
/chromosome="1"
172. .1347
                                                                                                                                                                                                                 /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                1340.
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                                                                                                                                                                                                                                                                /note="identified
                                                                                                                                                                                                                                                                                       /gene="DR0771"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                          codon_start=1/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="R1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="DR0770"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermus/Deinococcus group; Deinococcales; Deinococcus.
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                                                                                                                                                                                                                                                         by Glimmer2; putative"
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ALPLKFISAESALTALEKFEGEEKFETVISLDSNUKPFQTTRPFGKFGLPNSIKVIPD
SSNKRLIIGSNSEDGIRIRSFVETIDVQSSGKVISTDSISEIXIVRGQKESVLOFLAD
SFPELIVTDYASGGLAIEGPRTSVNRAIILLGQVDRAPEIPIVQRIYTVRQQAADITA
LLAAQXPTLRVTPVGQTGQLULNGAQAQLDTALALLEQVDRAPVAESRTVQRVFQLV
MASAEEVKATLEGTLARDLTADSNNDVLPNVPVTATDANGNTTVVSVPNALGKTANQG
TANAQAQTAQTPANTQQATLIADKRTNSILIVRGTPEQVAQVAELVPQLDQVPQLNVQ
VRIQEVNERALQSLGLNWRATFGGFNNAVSGGTGLATFNPTQSFLGFNIFPTLTALE
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TTTPGTTDESSGKKATGTAAKSQKGTQSGDGSDESLVATVPPLEGEGTATPPVPVPGG
INPDRPLKTLSGADPFGSLTPSPGTGTAGGTAPATVEAQTPETQSPETAPETQAPTA
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ITNKETTLAADQAKAARVPTLTAEVARLEVEREKFLRALPPTANFGQVVANLRQTVSA
AGGDLKTLNFAGSGAAGANLPAGVRPIGMTMSVNGRFPQLFQILRSLELQNRFTTVDN
VSLQTQGDAGTGGGGTLGSTLGLTVYTFDASGATSTPDAAAPAAGTPAPAAPAAGGTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="DR0774"
4620. .6842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPRVVTSPAAGVPAGNAAPAPTPPPVVAARVPQANTVPELVAQAGTSAAPATSGASAG
TGTAGQAGNDAAGTAALPPLITAVGSEAAPASTATADAGSSTPAAPAATALDRLLAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OSTINSPAPVVLSSPAGSSVSGOGGVLDYSSRLDQGALPTPVLPVSPTEVRSPTSAP
VSGSSVNGDSVGSGMATAPTVVVSTPAQPTTTPSASSRTARNTAGQSGAGQNTGASR
ASGTPSRASAPANVVVVRPPARVSGTSAAGATGSSRTGAAGTPAATTPTRNQSASGTRPA
SGQTPPRVIAVAPAGGARTPAAPGNRPATAAPTRPSPSSTAPSKTVVVRPPVLYSGOQ
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2709. .4616
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/protein_id="AAF10355.1"
/db_xref="G1:6458488"
                                                                                                                                                                                                                                                                                              /gene="DR0775"
6938. .8254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to Sp:001565 Sp:P31700 GB:X65265 PID:581156
percent identity: 48 99; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="DR0774"
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/db_xref="GI:6458489"
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/gene="DR0773"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TQGLTRRVYDGNVTMQSGQRSLSATGGAQNASSGAAASVKSGGRLEINIPSAAGNIVR
QIDYGLNLDFFSPQVAPDGTITLRIRGQVNQPATAITADSLPNLIDFTNSEAQSTITF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PITANVGKYVGPLSTFLASIAKSAGYEVVFNFNIDALALINGEIVFGNSTASVTTSYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product-"general secretion pathway protein D, putative"
/protein id-"AAF10350.1"
/db_xref="GI:6458483"
/translation-"MNKRHALLLTAVLGMATAYAQTAPTTTVNTLQTVYRDPSLTSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity; putative"
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                       /product="chorismate synthase"
/protein_id="AAF10351.1"
/db_xref="GI:6458484"
                                                                                                                                                                                                                                                                                                                                                                                                                            KNGQTILMSGLLGSTETTNRSGVPFLSSLPGVGAAFGEKRTEKTQSQLLVIITGTVVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
translation="MFVLALLAKKLCHLFVKCSTSYRRLSAKGRRFFDSRGGACLLKP/
                                                                                                                       /transl_table=11
                                                                                                                                                            codon_start=1
                                                                                                                                                                                           identified by sequence similarity; putative"
                                                                                                                                                                                                                             'note="similar to GB:AE000657 percent identity: 68.57;
                                                                                                                                                                                                                                                           /gene="DR0775"
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SOURCE
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                                                                                                        REFERENCE
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                                                                                                                                                                                                                                                                                     ACCESSION
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Best Local
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                                                     TITLE
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nes 27; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAACCACGCTCGCCGCCGATCAGGCCAAAGCGGCG 2232
Henriques,A.O., Beall,B.W., Roland,K. and Moran,C.P. Jr. Characterization of cotJ, a sigma E-controlled operon affecting polypeptide composition of the coat of Bacillus subtilis spores J. Bacteriol. 177 (12), 3394-3406 (1995)
                                                                                                                             Bacillus subtilis
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                AF012532 18622 bp DNA BCT 12-AUG-1997 AF012532 18622 bg LORA trpC2 YefA (yefA) gene, partial cds and YefB (yefB), YefC (yefC), YeeA (yeeA), YeeB (yeeB), YeeC (yeeC), YeeD (yeeD), YeeE (yeeE) and YeeF (yeeF) genes, complete
                                                                                                                                                                                                          Bacillus subtilis.
                                                                                                                                                                                                                                                             AF012532.1
                                                                                                                                                                                                                                                                                        AF012532
                                                                                                        (bases 15361 to 18622
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FVAASYLRGVAFYTAFTTLLGHVDAAVGGKTGVNLPEGKNLVGAFWPRAVWCDTATL
TTLDDAVFREGAABAFKHGLMADPSLLDRVVSSDFRPGGALLEDTLADD.1AVKAGVVT
RDLTEQGERAFLNFGHTLAHALEAVTHQAIPHGEAVAYGMHYAARLSHALGGADLTAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="DR0777"
8965. .10017
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/sglierpamvalagemgicksrigmelsralalhevdtdkiltrvvcksipbvpaq
egegyfracerevvqrvtrldhavislgggtfiheenrrlllsrgpvvvlmatpetvv
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VPAAGVILQCVIGWVLAEAITEKFGGDTLPELQERLAAARRYAAEY"
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PVGLGSFVHYDRKLDGKIAQACLSVQAMKGVEIGRAFENAVKPGSGVHDAIHYREGTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="3-dehydroquinate synthase"
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                                                                                                                                                                                                                                                                GI:2318058
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77.18;
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Location/Qualifiers
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Borriss,R. and Schroeter,R.

The 55-58 degree segment of the Bacillus subtilis chromosome, region spanning from the purA gene cluster to the cotJ operon
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1024 .1030
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1068 .1445
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                                   /gene="y
1520...4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to Enterococcus faecalis plasmid PY117 orf4
encoded by GenBank Accession Number D78257"
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similar to Chlamydia trachomatis Homl: SwissProt Accession
                                                                                                                                                                                              /gene="
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AINITNEDISNFETTLHQLSKDLEFQKIEKEIIDFKKSLDKFMKEGTLTPEMLHLLVD
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                                           -"yeeA"
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RBS

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complement (7490.

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gybylkgeglitygegytsalnevldtnkkyivhienderskokydevckild
gybylkgeglitygkrhsdgktlkiadlyddoverenvaylkniealddldiii
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GSMIQAVASEESRSYLGMHYTSYPNIKKVIKPLFLKLKNQSFLDAYDDYTKLEMLLTR
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DEVVTYTVNTMLKAISASLLMGQVLTPDFKFKRRNESEKSSTTGELFVKGLKEPSTE
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VRQHVVLDTVMKGAKSEVVGSKEFIRMADKFINIEDLDINLIDSINPFOKAFEVLSKE
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FGPLDTKVNKYLFVDETKKLYSNISPYLTDGENILVSSRTKFISSLPKLHEGNWENDG
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ELSTRRKNEIEEAILEILDLREEQGGTLAELYNPSTMPIELKVAHEKLDGIVERAYRQ
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NIIETNRGLDLFLIRLLFCFFAEDTDIFKRNSFTNLIKTLTEEDGSNLNKLFADLFIV
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hypothetical protein MJECS02 encoded by GenBank Accession
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                                                                                                                    PQISSIKNLYKIGFTTGSVENRIRNAENQSTYLYAPVEIVTTYQVFNMNASKFETAIH
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Best Local
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Azevedo, V., Bertero, M.G., Bessieres, P., Bolotin, A., Borchert, S., Borriss, R., Boursier, L., Brans, A., Braun, M., Brignell, S.C., Bron, S., Brouillet, S., Bruschi, C.V., Caldwell, B., Capuano, V., Carter, N. M., Choi, S. K., Codani, J.J., Connerton, I.F., Cummings, N. J., Daniel, R. A., Denizot, F., Devine, K. M., Dusterhoft, A., Ehrlich, S. D., Emmerson, P.T., Entian, K. D., Errington, J., Fabret, C., Ferrari, E., Foulger, D., Fritz, C., Fujita, M., Fujita, Y., Funa, S., Galizzi, A., Galleron, N., Ghim, S.Y., Glaser, P., Goffeau, A., Golightly, E.J., Grandi, G., Guiseppi, G., Guy, B.J., Haga, K., Haiech, J., Harwood, C. R., Henaut, A., Hilbert, H., Holsappel, S., Hosono, S., Hullo, M. F., Itaya, M., Jones, L., Joris, B., Karamata, D., Kasahara, Y., Klaerr-Blanchard, M., Klein, C., Kobayashi, Y., Koetter, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus subtilis
813890.
                                                                                                                                                                                                                                                                                                                       Kunst,F., Ogasawara,N., Moszer,I., Albertini,A.M., Alloni,G
                                                                                                                                                                                                                                                                                                                                                                Bacillus/Staphylococcus group; Bacillus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus subtilis.
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/gene="yeeD"
8277. .8298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="similar to Bacillus subtilis orf94 hypothetical
59.7 kDA protein in CWLA-CISA intergenic region: Swiss
Accession Number P45942"
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complement(9464. .9470)
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KALSKKPPKKVAVQIEPVYSGDSLRPSYFDVTYKIGSRKEISVSIKISLGVRRMETRK
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/gene="yeeE"
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/product="YeeE"
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/note="rho independent terminator; deltaG= -10.2kcal/mol"
/citation=[2]
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LQSSDGKfEEDLSKvrnkLDTLTrayLESanDymnpmlkemhktekLLkeyDettQS"
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/db_xref="GI:2318064"
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Pred. No. 5e+02;
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MEDLINE
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Submitted (18-NOV-1997) I. Moszer, A. Danchin, Institut Pasteur, Regulation de 1'Expression Genetique, 28 rue du Docteur Roux, 7577
Paris Cedex 15, FRANCE. E-mail: moszer@pasteur.fr, Paris Cedex 15, FRANCE. E-mail: description of the control o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Purnelle,B., Rapoport,G., Rey,M., Reynolds,S., Rieger,M., Rivolta,C., Rocha,E., Roche,B., Rose,M., Sadaie,Y., Sato,T., Scanlan,E., Schleich,S., Schroeter,R., Scoffone,F., Sekiguchi,J., Sekowska,A., Seror,S.J., Serror,P., Shin,B.S., Soldo,B., Sorokin,A., Tacconi,E., Takagi,T., Takahashi,H., Takemaru,K., Takeuchi,M., Tamakoshi,A., Tanaka,T., Terpstra,P., Tognoni,A., Tasato,Y., Uchiyama,S., Yandenol,M., Vannier,F., Vassarotti,A., Viari,A., Wambutt,R., Wedler,B., Wedler,H., Weitzenegger,T., Winters,P., Wipat,A., Yamamoto,H., Yamane,K., Yasumoto,K., Yata,K., Danchin,A., Yoshikawa,H.F., Zumstein,E., Yoshikawa,H. and Danchin,A., Yoshikawa,H.F., Zumstein,E., Yoshikawa,H. and Danchin,A., Yoshikawa,H.F., Zumstein,E., Yoshikawa,H. and Danchin,A.
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Lardinois,S., Lauber,J., Lazarevic,V., Lee,S.M., Levine,A.,
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IAVNOGERIDIELIMOGEIIENNLKONRLTESWLLEELRKRDIKVKETVYAVLLGNGD
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33. .740
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/gene="ydgA"
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33. .740
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/transl_table=11
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Bacillus subtilis"
                                                                                                                                                                                                                                                            function="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Krogh,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'ydfs"
                                                                                                                                                                                                         to hypothetical proteins from B. subtilis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           .1441)
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3117. .3
                                                                                                                                                                                                               complement(3705. .5393)
/gene="expZ"
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2610. .
                                                                                                                                                                                         complement(3750. .5393)
                                                                                                                                                                                                                                                                                      complement(3705.
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3117. .3590
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2026..
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                                                                                                                                                                                                                                                                                                                                    QAYENMIPNGRDSSNHYFWNITNDQGERMGWLWLYADPLHPQKEAFIYSFGLYEAFRG
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/gene="ydgB"
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GDLSPTSSLLNTGNIDSDVSDQDQIGNPSAPISNQI"
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/function="unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MKSKGVESRKRLLKAAANEFSVRGFHDAKVSEIVKKAGFTQPSF
YLYFQSKEAIFAELITDFHSRVRKLTESLLLENGLNTEDVSKRVLLAVETVFQFLDED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2026
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                                                                                                                     transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="similar to hypothetical proteins"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="MISIMMKVSLAVFMLAGGIIKVSRVPFQVEHWRHYQYPLWFLTV/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="SPTREMBL:P96702"
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QΥ

Matches

VERSION KEYWORDS

ACCESSION

AE004219

Locus

SOURCE

REFERENCE

AUTHORS

REFERENCE

AUTHORS JOURNAL TITLE

JOURNAL

Direct Submission Submitted (14-JUN-2000) The Institute for Genomic Research, Medical Center Dr, Rockville, MD 20850, USA

Mekalanos, J.J., Venter, J.C. and Fraser, C.M.

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Db 154535 TCAGAGTTTGCGGCTGCTCATGCTGCATATTGGACCTCATTTT 154577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
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Best Local :
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                                                                                                                                                                                                                                                                                       Heidelberg, J.F., Eisen, J.A., Nelson, W.C., Clayton, R.A., Gwinn, M.L., Dodson, R.J., Haft, D.H., Hickey, E.K., Peterson, J.D., Umayam, L.A., Gill, S.R., Nelson, K.E., Read, T.D., Tettelin, H., Richardson, D., Ermolaeva, M.D., Vamathevan, J., Bass, S., Qin, H., Dragoi, I., Sellers, P., McDonald, L., Utterback, T., Fleishmann, R.D., Nierman, W.C., White, O., Salzberg, S.L., Smith, H.O., Colwell, R.R., Mekalanos, J.J., Venter, J.C. and Fraser, C.M.
2 (bases 1 to 11936)
Heidelberg,J.F., Eisen,J.A., Nelson,W.C., Clayton,R.A., Gwinn,M.L.,
Bodson,R.J., Haft,D.H., Hickey,E.K., Peterson,J.D., Umayam,L.A.,
Dodson,R.J., Haft,D.H., Read,T.D., Tettelin,H., Richardson,D.,
Gill,S.R., Nelson,K.E., Read,T.D., Tettelin,H., Richardson,D.,
Ermolaeva,M.D., Vamathevan,J., Bass,S., Qin,H., Dragoi,L.,
Sellers,P., McDonald,L., Utterback,T., Fleishmann,R.D.,
Sellers,P., McDonald,L., Utterback,T., Smith,H.O., Colwell,R.R.,
Nierman,W.C., White,O., Salzberg,S.L., Smith,H.O., Colwell,R.R.,
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                                                                                                                                                                                                                                                                   cholerae
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1 (bases 1 to 11936)
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                                                                                                                                                                                                                                  Nature 406, 477-483 (2000)
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ALIKVIAILALIVIGLVMIFKGFSTSSGVSSFTNLWSHGGLFPNGMHGFILSFQMVVF
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VRFSIDTTHKTGKRFLEVQNVTKAFGERTLFKNANFTIQHGEKVAIIGPNGSGKTTLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(5428.
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LGFTAAQWTEPIKHMSMGERVKIKLMAYILEEKDVLILDEPTNHLDLPSREQLEETLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QYSGTLLAVSHDRYFLEKTTNSKLVISNNGIEKQLNDVPSERNEREELRLKLETERQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GI:9655899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 22.2; DB 2;
Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to amino acid ABC transporter (permease)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .7089)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CT 31-JUL-2000 of 251 of the complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 213190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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CDS

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FEATURES
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                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                                             GLEHRRTRHGQDLWLEATYNPIFNDAGVVTQVVKFASDVTDQVLKAHATKEASQMAQQ
TSAETVRVAESGREMIDAAATIASGITESIAGANALMTDLSSQSQRITQIVTTINKIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="VC1405"
460. .2247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                460.
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3824. .5017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="VC1406"
2326. .3642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LANEMAEGNFSKRAKYTTGDEIGQLITSMNTMAQSLSHIVGEVIDRANTIASTVTQLA
SSAESNKKSVQQQQANTEQVTSAMAQMAITITEVASSAEESSAATARAQENARYSCDV
LGKTETVSSQLVANAQQSQQNIVELEASTRQIESFVLVVEGISEQTNLLALNAAIEAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to GB:X61367 PID:48195; identified by
sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(98. .220)
/gene="VC1404"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="biotype: El Tor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAQETAQASEELAQQAQGLKLLMGRFVIS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RAGEQGRGFAVVADEVRALASRSQQATHEIKGLIQTLVERAQSATKMIDSSDRQIEES
FSSTTAAKKQLDSINLALLELTSANTQVAAASEEQSVAADEISHNMTDIRDAGETIML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="methyl-accepting chemotaxis
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                                                                                                                                                                                                                                                       /gene="VC1407"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="VC1406"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MENLEIQEQTIIKISTKNIDADLAQILFPILNKNKVNPCF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Vibrio cholerae"
/strain="N16961"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                     transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'db_xref="taxon:666"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3642
                                                                                                                                                                                                                          identified by sequence
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KSLAVFGGVDEQAQKQRLIDGVDVLVATPGRLMDLYGQRAVYFEEIEMVVLDEADRWL DMGFIESINKIIDCLPSEVQFLLESATLSRKVRELAKTAVRDEEISTAANAASKSUL SOMGFIESINKIIDCLPSEVQFLLESATLSRKVRELAKTAVDLEETSTAANAASKSUL SOMLITVDKDTKSALLSHLINEQWDQALIFIETKHGAAKLVSQLEKGIHAAEAFHSG RSQALRAQLLEDFKSGKIKYLVATGVAARGIDIDQLSRVVNYDLPFFADEYVHRIGRT GRAEAVGEAISFVSKDNFKNLCMIESRLGHLIERRVVEGFEPKKPVPISILNYVPKHK
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8450. .9985
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okanaaltdnttydsnpevllakaryeqakidlertvirapisgivakrqvqvgrrvq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EANELSSTNTFSHOAEMDWPSANWWORYQDAQLNHLIEEALQHSPSLEMAMARLKGAQ
GFARQAAIRSFDLGLAASATESKVSERYQSATPDGWWDYGTLYLNFQYDPDFWGKN
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LLEKRYANGLETLGSVSQAKAVAASVEAELLGIQESIQLQKNALAALVGQGPDRAASI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="VC1409"
5785. .7239
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similarity; putative"
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                                                                                                                                                                                                                                                                                                                                                                                  VGMPLMTVVPTDHIIVDANFKEVELRDVKVGQPVTLTADLYGDDVTYHGVVAGFSGGT
GSAFSMIPAQNATGNWIKVVQRLPIRIELDPKDLQAYPLQVGLSMVATIDTAGTTDPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LNNQRALVNLQSRAFSLDLALIHALGGGFETTES"
7220. .8440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEPHITLTSRYGLPSEAGVGLLGHRADITAARWRAEAAAQQVGIAQAQFYPDVTLSAF
IGYQAFGLDHLFDSGNDAGAIGPAIYLPLFTGGRLEGQLTSAEARYQEAVAQYNGTLV
QALYEVADVVTSSQALQARINKTEQAVQQAEQALHIATNRYQGGLATYLDVLVAEESL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product-"multidrug resistance protein, putative"
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7220. .8440
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                                                                 protein
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CDS

/translation="MSHNADNEMQPLSGWALFFGALCLAMANFLAILDTTIANVSVSN

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Search completed: March 4, 2001, 12:03:42 Job time: 5597 sec
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                                                                                                                                                                                                                                        Query Match
Best Local S
                                                                                                        gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                  / Match 48.9%; Score 22; DB 1; Le
Local Similarity 73.7%; Pred. No. 6.2e+02;
nes 28; Conservative 0; Mismatches 10;
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939. 10055
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complement(10060. .11796)
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LANSMTILVMFRYLLGFVGGPLMPLSQTLMIRIFPKNKSHAAIGIWSMTTLVAPIMGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .10055
                                                                                                                                                                                                                                                  Length 11936;
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

March 4, 2001, 10:32:15; Search time 106.76 Seconds (without alignments) 67.930 Million cell updates/sec Run on:

US-09-101-423B-7

Title: Perfect score: Sequence:

1 aatccaagcttgcggccgat.........cgaatatgcggccgcattat 45

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

280836 seqs, 80580151 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued\_Patents\_NA:\*

1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*
4: /cgn2\_6/ptodata/2/ina/6\_COMB.seq:\*
4: /cgn2\_6/ptodata/2/ina/pcyncs\_COMB.seq:\*
5: /cgn2\_6/ptodata/2/ina/pcyncs\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description		, 'I	76,	26,	2, 1	Sequence 1, Appli	Segmence 1 Appli	ì -	10	٦ ,	Datont No 5222571	٠.	<u>,</u>	1 , 7	٦,	16,	'n.	6	e,	Sequence 3, Appli	1	o,	13,	. , ,	Sequence 5. Appli	-	, C	)   	Sequence 3, Appli	Sequence 1, Appli	
COLUMNITES	ID	IIS-09-136-251-1	-08-200-900	9 (	7	US-U8-948-/US-2	05-08-054-07/C-1	US-08-469-667-1	PCT-US95-07289-1	US-09-320-878-19	US-08-839-581A-21	5332671-12	PCT-US95-02481-3	- 1	US-08-706-037-16	TS-00-00E-307-16	TC-00-33E-400-1	T-60#-666 60 60:	12-08-403-634 3	US-V0-4U3-034-3	US-UB-913-441B-3	US-08-907-229-1	US-U8-258-420-9	US-08-850-961-13	US-08-042-747A-7	US-09-011-745-5	US-08-406-248-1	PCT-US94-09700-10	US-08-241-766-3	US-08-154-915-5	US-07-970-462A-1	
	Length DB	3481 3	41 1	41 4		3415	T 0.110	638 1	638 4	38506 3	37 2	62 5		8051 2	88	288	68750 3		1424		1424	1001	1 200	2001	2943 I	6028 3	495 1	1194 4	1721 1	2100 1	2106 1	
æ	Query Match	47.1	45.3	45.3		44.0		47.7	42.2	41.8	41.3	41.3	41.3	41.3	40.9	40.9	40.9	40.4	40.4		* •	7.	* * *	4.04	40.4	40.4	40.0	40.0	40.0	40.0	40.0	
	Score	21.2	20.4	20.4	20.2	8 6 1	1	61	19	18.8	18.6	18.6	18.6	18.6	18.4	18.4	18.4	18.2	18.2	18.5	18.6	10.2	9	7.07	70.7	7.07	30 ·	18	18	18	18	
	Result No.	c 1	0	3	4	C N	,	o t	~ 0	30	6	10	c 11		13	14	15	16	17	æ -	0 -	5 5	9 5	22	2.5			C 72	36	c 27		

ZIP: 02140 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 22, Appli Sequence 22, Appli Sequence 22, Appli Sequence 22, Appli Sequence 22, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli		3; Length 3481; 8; Indels 0; Gaps 0; AND METHOD OF USE 1 Affairs
06 4 PCT-US92-10904-1 06 4 PCT-US94-09700-1 21 1 US-08-54-043A-1 21 2 US-08-75-015-1 21 4 PCT-US94-12936-1 45 2 US-08-61-1886A-1 45 2 US-08-61-22 14 1 US-08-20-812-2 14 1 US-08-920-812-2 14 1 US-08-920-822-2 14 1 US-08-920-822-2 14 1 US-08-920-822-8 14 1 US-08-920-828-2 14 1 US-08-920-828-2 14 1 US-08-920-828-2 15 US-08-920-828-2 16 US-08-920-828-2 17 US-08-920-828-2 18 US-08-920-828-2 19 US-08-920-828-2 10 US-08-920-828-2 11 US-08-929-148A-8 11 US-08-484-054-8	ALIGNMENTS  on US/09136251A  Taro Taro Suko Hasako Ho. 6127156ibumi P. SORBITOL DEHYDROGENASE GENE Dital Dehydrogenase Gene UMBER: US/09/136,251A 1998-08-19 1997-08-21  rr. 2.1  ter suboxydans	1.2; DB to 11; atches agc 37 fl CGC 355 CGC 35
C 29 18 40.0 2106 C 31 18 40.0 2106 C 32 18 40.0 2121 C 33 18 40.0 2121 C 34 18 40.0 2121 C 35 18 40.0 2121 C 37 18 40.0 2245 C 37 18 40.0 6914 C 38 18 40.0 6914 C 39 18 40.0 6914 C 40 18 40.0 6914 C 40 18 40.0 6914 C 41 17.8 39.6 981 45 17.8 39.6 981	ESULT  1 - 136-251-1/C  Patent No. 612/156  GENERAL INFORMATION:  APPLICANT: HOSHINO,  APPLICANT: OJIMA, Set  APPLICANT: TOMIYAMA,  TITLE OF INVENTION:  CURRENT FILING DATE:  CURRENT FILING DATE:  EARLIER APPLICATION NEARLIER APPLICATION NEARLIER APPLICATION SERLIER APPLICATION NEARLIER APPLICA	Ouery Match Best Local Similarity 76 Matches 26, Conservativ 76 A ccaagcttggggcgate 4 ccaagcttggggcgate 1
	α D	A G BB

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APPLICANT: Chen, Yao-Tseng
APPLICANT: Chen, Yao-Tseng
APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Lisabeth
APPLICANT: Stockert, Loyd J.
TILSOR INVENTION: ISOLATED NUTH COLON CANCER AND METHODS FOR DIAGNOSING AND
TITLE OF INVENTION: ASSOCIATED WITH COLON CANCER
FILLE OF INVENTION: TREATING COLON CANCER
FILLE REFERENCE: LUD-5506-JEL/NUH
CURRENT APPLICATION NUMBER: US/08/948,705A
CURRENT APPLICATION DATE: 1997-10-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASTERQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS ADDRESSEE: CUSHMAN STREET: 130 WATER STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CALT: 0.4109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: DATE: DC-DOS/MS-DOS
SOFTWARE: PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTING SYSTEM: DATA:
APPLICATION NUMBER: US/08/054,077C
FILING DATE: 27-APR-1993
CLIASIFICATION: DATA:
APPLICATION NUMBER: US 07/694314
FILING DATE: 01-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S:
RESISTATION NUMBER: 34235
RESTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 40937
TELECOMMUNICATION INDERER: 34.000
                                                                                                                                                                                                                                                                                                                                                                                     Score 20.2; DE; DE; Pred. No. 25; O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 2715 ggtggggggggcgaacaggcccaagctgcggcagc 2747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEEX: 200291 STRE UR
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                            44.98;
APPLICANT: Scanlan, Matthew J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 3415 base pairs
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Best Local Similarity 75.89
Matches 25; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MASSACHUSETTS
                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Homo Sapiens
US-08-948-705-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                                                                                                        2885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                            SOFTWARE: I
                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
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0
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 20.4; DB 4; Length 41; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 20.4; DB 1; Length 41;
Pred. No. 13;
0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US94/00616
             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 71.1%; Pred. No. 13;
Matches 27; Conservative 0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 gcttgcggccgatcaggccgaatatgcggccgcattat 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 gottgcggccgatcaggccgaatatgcggccgcattat 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 GCTTGGACTTAACCAGGCTGAACTTGCGGCCGCATTCT 4
                                                                                                                                                                          NAME: Melnert, Maureen C.
REGISTRATION NUMBER: 31,54
REGISTRATION NUMBER: 31,54
TELECOMMUNICATION INFORMATION:
TELEPAN: (617) 876-1170 X8574
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/200,900A
FILING DATE: 23-FEB-1994
CLASSIFFCATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 26, Application PC/TUS9400616 GENERAL INFORMATION: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08948705A Patent No. 6043084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.3%;
71.1%;
                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 45.39
Best Local Similarity 71.19
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 41 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                   FILING DATE: 23 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ULT 3
-US94-00616-26/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCT-US94-00616-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-200-900A-26
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US-08-469-667-1

Sequence 1, Applic Patent No. 5733748

Application US/08469667

GENERAL INFORMATION:

APPLICANT:

Rosen, Craig

Yu, Guo-Liang

CORRESPONDENCE ADDRESS:

TITLE OF INVENTION: Colon Specific Genes and Proteins NUMBER OF SEQUENCES: 24

ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi ADDRESSEE: Stewart & Olstein

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

COUNTRY:

USA

Ŋ

07068-1739 Roseland

STREET:

6 Becker Farm Road

COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

PatentIn Release #1.0, Version #1.30

US-08-054-077C-1

NAME/KEY: LOCATION:

337..2733

FEATURE:

LOCATION:

406..2733

Best Local Similarity Matches 27; Conserv

Conservative

44.0%;

Score 19.8; DB 1; Length 3415; Pred. No. 36; 0; Mismatches 12; Indels 0

0

2153 CCACGCTCGCTGCAGATCTGGCCATCTCTGCCCCCGGCAT 2115

4 ccaagettgeggeegateaggeegaatatgeggeegeat 42

Query Match

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                                              Matches
                                                       Local Similarity
          agcttgcggccgatcaggccgaatatgcg 35
 AGCTGGCTGCCSACCAGGCCGTGTATGTG 36
                                              Mismatches
                                               6
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; NAME/KEY: ; LOCATION: US-08-469-667-1

NAME/KEY: LOCATION: FEATURE:

mat\_peptide 1..501

MOLECULE TYPE: FEATURE:

TOPOLOGY: STRANDEDNESS: LENGTH:

linear CDNA single INFORMATION FOR SEQ ID NO: 1:

TELEPHONE: 201-994-1744

SEQUENCE CHARACTERISTICS:

nucleic acid

638 base pairs

TELECOMMUNICATION INFORMATION: TELEPHONE: 201-994-1700

ATTORNEY/AGENT INFORMATION:

FILING DATE: 00 CLASSIFICATION:

APPLICATION NUMBER: US/08/469,667 FILING DATE: 06-JUN-1995

NAME: Ferraro, Gregory D. REGISTRATION NUMBER: 36,134 REFERENCE/DOCKET NUMBER: 32

25800-435

CURRENT APPLICATION DATA:

SOFTWARE:

Query Match

42.28;

Score 19; Pred. No.

60;

DB 1; Length 638;

0;

Gaps

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0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
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GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Rosen, Craig
                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: ASHLEY, Gary
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Mary C.
APPLICANT: MCDANIEL, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19, Application US/09320878A Patent No. 6117659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
CURRENT APPLICATION NUMBER: US/09/320,878A CURRENT FILING DATE: 1999-05-27 EARLIER APPLICATION NUMBER: CIP OF 09/141,908
                                                                                                               TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE FILE REFERENCE: 300622002120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                              APPLICANT: TANG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Colon Specific Genes and Proteins NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 638 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
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CITY: F
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TELEPHONE: Z
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 07068-1739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 36,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 0 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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75.9%;
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US-08-839-581A-21
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Best Local Similarity
~~+~hes 26; Conserv?
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 21, Application US/08839581A Patent No. 5958705
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EARLIER FILING DATE: 1999-02-08
EARLIER APPLICATION NUMBER: 60/100,880
EARLIER FILING DATE: 1998-09-22
EARLIER FILING CATE: 1998-09-22
EARLIER FILING DATE: 1998-05-28
EARLIER FILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                        TELEFAX: 312-474-0448 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EARLIER FILING DATE: 1998-05-06
EARLIER APPLICATION NUMBER: CIP OF 08/846,247
EARLIER FILING DATE: 1997-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EARLIER APPLICATION NUMBER: CIP OF 09/073,538
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                                   MOLECULE TYPE:
                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Young J. Suh
REGISTRATION NUMBER: P-41,337
REFERENCE/DOCKET NUMBER: 27866/33886
                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 37 base pairs
                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Staunton, Donald E.
APPLICANT: Lipsky, Brian P.
TITLE OF INVENTION: Cytoplasmic Modulators of Integrin
TITLE OF INVENTION: Binding/Signaling
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 233 SC
CITY: Chicago
                                                          TOPOLOGY:
                                                                    STRANDEDNESS: single
                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                  DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/839,581A
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                                                                                         nucleic acid
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                                                                                                              37 base pairs
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                                                          linear
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3 South Wacker, 6300 Sears Tower
              other nucleic acid
/desc = "primer"
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5332671-12
; Patent No. 5332671
; APPLICANT: FERRARA, NAPOLEONE; LEUNG, DAVID W.H.
; TITLE OF INVENTION: PRODUCTION OF VASCULAR ENDOTHELIAL CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
PCT-US95-02481-3/c
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Best Local Similarity
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Best Local 9
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                          REFERENCE/DOCKET NUMBER: 01 TELECOMMUNICATION INFORMATION:
                                                                      APPLICATION NUMBER: 08/202,909
FILING DATE: February 28, 1994
ATTORNEY/AGENT INFORMATION:
NAME: ROXANDE Edwards Cenatempo
                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02481
                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/07/389,722
FILING DATE: 04-AUG-1989
PRIOR APPLICATION NOMBER: 369,424
FILING DATE: 21-JUN-1989
APPLICATION WHEER: 351,117
FILING DATE: 12-MAY-1989
                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                 COMPUTER: MacIntosh
OPERATING SYSTEM: 7.0
SOFTWARE: Microsoft Word
              TELEPHONE:
                                                            REGISTRATION NUMBER:
                                                                                                                                                                       FILING DATE
                                                                                                                                                                                                                                                                                                                               STATE:
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                                                                                                                                                                                                                                                                                                                COUNTRY: USA
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nes 21; Conserva
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404-818-3799
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Satterlee, Daniel G.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Methods of Determining the Gender of Poultry
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84.0%;
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Pred. No. 64;
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Pred. No. 60;
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                                                            Matches
                                                                             Query Match
Best Local :
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SEQUENCE CHARACTERISTICS:
LENGTH: 1708 base pairs
TYPE: nucleic acid
STRANDENNESS: single
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                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
6190 TGCGGCCGAACAGGTCGAGCAGGTGGGCGAACT 6158
                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 58
TELECOMMUNICATION INFORMATION:
TELEPHONE: (847) 938-3137
                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 21-DEC-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Staver, M.J.
TITLE OF INVENTION: POLYKETIDE-ASSOCIA
TITLE OF INVENTION: BIOSYNTHESIS GENES
                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       260 CCCTGCCTGCAGCAGATCAGTCCACATCTGTCTCCTCGTTA 220
              11 tgcggccgatcaggccgaatatgcggccgcatt 43
                                                                                                                                                                LENGTH: 8051 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity nes 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                         Local Similarity
                                                                                                                                                                                                                                                                  TELEFAX:
                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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3, 5998194
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                                                                                                                                                                                                                                                                                                                                               Dianne Casuto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Illinois
                                                                                                                                                                                                                                                                 (847) 938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Katz,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Katz, L.
Donadio, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Summers, R.G.
                                                            Conservative
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                                                                         41.3%;
72.7%;
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Pred. No. 95;
                                                                         Score 18.6; DB 2;
Pred. No. 1.1e+02;
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                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 1708;
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                                                                                        Length 8051;
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; TOPOLOGY: li;
; MOLECULE TYPE:
US-08-706-037-16
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US-08-706-037-16
                                                                                                                                                                                                                       US-09-005-397-16
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                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                    Patent No. 5972670 GENERAL INFORMATION:
                                                                                                                                                                               Sequence 16, Appric
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Patent No. 5770419
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                Matches
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APPLICANT: Xu, Fe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
                                  APPLICANT: Xu, Feng
APPLICANT: Berka, Randy M.
APPLICANT: Wahleithner, Jill A.
APPLICANT: Wahleithner, Jill A.
APPLICANT: WANTION: BLUE COPPER OXIDASE MUTANTS WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 45
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US |
FILING DATE: 1-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/706,037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1-SEP-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Berka, RAPPLICANT: Wahleith TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
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CITY: New York
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CITY:
              STREET:
                                                                                                                                                                                                                                                                                             20 AATTCAAGCTTGTCGACGTTTAAACCAAATTTGAGATCTCTTAA 63
                                                                                                                                                                                                                                                                                                                     1 aatccaagcttgcggccgatcaggccgaatatgcggccgcatta 44
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New York
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                                                                                                                                                                                                      Application US/09005397
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         405 Lexington Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Berka, Randy M.
Wahleithner, Jill A.
WENTION: BLUE COPPER OXIDASE MUTANTS WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             212-878-9655
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                              No. 5972670o No. 5972670disk of No. 5972670th America,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38,711
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Pred. No. 79;
                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                64th Floor
                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
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                                Inc.
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COUNTRY: United States of America ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

STATE: N COUNTRY:

New York

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APPLICANT: Cyr, Devon

APPLICANT: Goerlach, Joern

TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES

FILE REFERENCE: 4-30582A

CURRENT APPLICATION NUMBER: US/09/335,409

CURRENT FILING DATE: 1999-06-17

NUMBER OF SEQ ID NOS: 30

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1

LENGTH: 68750

TYPE: DNA

ORGANISM: Sorangium cellulosum

US-09-335-409-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Harrington, James J.
REGISTRATION NUMBER: 48.711
REFERENCE/DOCKET NUMBER: 45.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEPHONE: 212-878-9655
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 88 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
-US-09-005-397-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09335409 Patent No. 6121029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 40.9%; Score 18.4; DB 2; Length 8 Best Local Similarity 63.6%; Pred. No. 79; Matches 28; Conservative 0; Mismatches 16; Indels
                                                                        Query Match 40.9%; Score 18.4; DB 3; Length 68750; Best Local Similarity 78.6%; Pred. No. 1.7e+02; Matches 22; Conservative 0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: 21rkle, Ross
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/706,037
FILING DATE: 30-AUG-1996
APPLICATION NUMBER: US 60/002,800
FILING DATE: 1-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
13 cggccgatcaggccgaatatgcggccgc 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 AATTCAAGCTTGTCGACGTTTAAACCAAATTTGAGATCTCTTAA 63
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В 36360 cggccgggcagtccaactatgcggcggc 36387

Search completed: March Job time: 5582 sec 4, 2001, 12:05:17

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title:
Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N_Geneseq_36:*
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Copyright (c) 1993 - 2000 Compugen Ltd.
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/cgn2_2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
/cgn2_2/gcgdata/geneseq/geneseqn/NA1982.DAT:*
/cgn2_2/gcgdata/geneseq/geneseqn/NA1983.DAT:*
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20.4	20.4	20.4	20.4	20.8	20.8	20.8	20.8	21.2	21.2	21.4	45	Score		
45.3	45.3	45.3	45.3	46.2	46.2	46.2	46.2	47.1	47.1	47.6	100.0	Match Length	O a	•
4380	4260	939	41	9181	8907	7647	1503	3481	500	42	45	Length		
9	9	21	15	20	21	19	19	20	20	18	18	DB		
N80222	N81768	Z29251	Q70114	X84323	Z36926	V15519	V15518	X21501	X91235	T61221	T72784	ID		SUMMARIES
Sequence of Mycoba	Sequence encoding	Rifin 3193 gene	Lambda INNER prime	Stealth virus nucl	Nucleotide sequenc	Hamster oral papil	Hamster oral papil	DNA sequence of so	T. gondii immunoge	Primer HUCKN.NOT f	DNA tag. Syntheti	Description		

4.4	C 43	c 42						36	35	34	ω ω	32	31	30	29	28	27	26	c 25	24	2 3	22		c 20				16	1.5	c 14	
18.8	10.00	18.8	18.8	18.8	18.8	18.8	19	19	. 19	19	19	19	19	19.2	19.2	19.2	19.2	19.4	19.4	19.4	19.4	19.4	19.4	19.6	19.8	19.8	20	0	0	20.2	0
41.8	41.8		41.8		41.8		•	•	•		•	•	•	•		•					43.1							٠	4.	44.9	45.3
13842	7059	4248	2465	2465	2302	2302	5474	4394	1218	1173	638	. 638	417	1842	1095	834	619	2352	753	546	546	524	424	3183	7673	3415	2178	5398	2885	1818	4380
21	) 15	21	21	18	21	21	16	13	20	20	19	18	20	21	21	21	21	21	21	21	20	21	20	20	19	17	20	12	20	21	19
X12962 Z87297	Q55004	A27364	A15620	T58086	A15622	A15621	Q90251	Q21604	X91630	X91764	V16668	T45880	V90226	Z56349	254498	Z53639	Z53637	Z54296	Z53374	Z53377	Z12160	Z53380	X84148	X26611	V58229	T36481	Z12261	Q13284	X40055	Z46842	V05708
Enterococcus faeca S. venezuelae macr	i-cr	hizobi	heat shock	heat shock	heat shock	Human heat shock p	Tuberous sclerosis	Alpha galactosidas	Porphorymonas ging	Porphorymonas ging	Polynucleotide sea	Human colon specif		⊢.				מ			Neisseria gonorrho	Neisseria gonorrhe	DNA encoding human	Trypanosoma cruzi	Omega-cyclohexane	Human integrin bet	Neisseria gonorrho	P.denitrificans co	വ		Mycobacterium tube

## ALIGNMENTS

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FILELL
                                                                                                                                                                                                                           RESULT 1
T72784
Barraclough BR, Rudland PS;
                                                                                                                                                                                                 misc_feature
                          (UYLI-) UNIV LIVERPOOL.
                                                    10-JAN-1996;
                                                                             10-JAN-1997;
                                                                                                                                 WO9725443-A1.
                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                    Metastasis-inducing DNA; Met-DNA; cancer; diagnosis; ds
                                                                                                                                                                                                                                                                                                                                                                                     T72784;
                                                                                                       17-JUL-1997.
                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                               DNA tag.
                                                                                                                                                                                                                                                                                                                                                                                                           T72784 standard; DNA; 45 BP.
                                                                                                                                                                                                                                                                                                                                                           22-SEP-1997
                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                   96GB-0000470.
                                                                             97WO-GB00074.
                                                                                                                                                                                               /*tag= a
/note= "5' single stranded overhang"
45
                                                                                                                                                /*tag= b
/note= "5' overhang on complementary strand of 4
/note= "5' overhang on complementary strand of 4
                                                                                                                                                                                                                                          Location/Qualifiers
1..2
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WPI; 1997-372878/34.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  into a syngeneic animal, injecting the transformed cells into a syngeneic animal, selecting those animals having metastasing tumours, and recovering the Met-DNA (see also T72785-90) from them. The human DNA is tagged to assist in its removal or insertion from or into a host or vector. The tagging procedure overcomes the problem of identifying the inserted human DNA sequences in the rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         metastasis-inducing DNA (Met-DNA). This method involves transferring the human DNA into a cell line (pref. rat Rama 37) that produces only benign, non-metastasing tumours when injected that produces only benign, non-metastasing functions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A DNA tag (T72784) having HindIII, SfiI, NotI and a defective HindIII site is used to tag human DNA from malignant, metastatic cancer cells in a novel method of screening and recovering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated metastasis-inducing DNA - used to develop products to
The present sequence is a primer for the PCR amplification of the CDNA encoding an immunoglobulin (Ig), light chain, constant region. The primer can be used in a novel method for the production of recombinant antibodies, comprising the selection of B cells from a lymphocyte fraction, isolation of mRNA from individual B cells,
                                                                                                                                          prodn. of recombinant antibodies - by amplification, cloning and
expression of cDNA generated from B-cell mRNA
                                                                                                                                                                                              WPI; 1997-088250/09.
                                                                                                                                                                                                                                                                                                                                  20-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                   23-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                     DE19526546-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Primer; polymerase chain reaction; PCR; amplification; light chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Primer HUCKN.NOT for light chain constant region cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T61221 standard; DNA; 42 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 45 BP; 11 A; 13 C; 12 G; 9 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genome of the transfected cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 identify and treat patients at risk from metastatic tumours
                                                                                                                                                                                                                                                                (OPEL/) OPELZ G
                                                                                                                                                                                                                                                                                                  20-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       recombinant; antibody; B cell; diagnosis; therapy; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunoglobulin; Ig; constant; region; production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aatccaagcttgcggccgatcaggccgaatatgcggccgcattat 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                         Page 11; 11pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
llarity 100.0%;
Conservative (
                                                                                                                                                                                                                                  Welschof M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                  95DE-1026546
                                                                                                                                                                                                                                                                                                                                    95DE-1026546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 45; DB 18; Pred. No. 7.7e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                       region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Ωy DЬ

473 AATGTTCCAGCCGATCGGGCCGAACTTGCGGCGG 440

6 aagcttgcggccgatcaggccgaatatgcggccg 39

Matches

Conservative

0,

8;

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                                                                                                                                                         PPA XXX PPA XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                          Query Match
Best Local
                                                                                                                                                                                                      The invention provides isolated Toxoplasma gondii nucleic acids that encode immunogenic polypeptides. The T. gondii nucleic acid molecules, immunogenic proteins and antibodies to the proteins can be used to inhibit T. gondii occyst shedding in a cat due to infection with T. gondii. They can be used for preventing T. gondii infection and for preventing the spread of T. gondii infection. They can also be used for detection T. gondii infection They can be used for preventing the spread of T. gondii infection method can be used to detect parasite cysts or oocysts in feces, e.g. from enteric apicomplexa oocysts such as Cryptosporidium oocysts and Toxoplasma oocysts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        reverse transcription of the mRNA into cDNA, amplification of the cDNA by PCR and cloning and expression of the cDNA. The recombinant antibodies can be used for diagnosis and/or therapy, while the method avoids the need for intermediate separation of light and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T. gondii immunogenic protein encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X91235 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 42 BP; 11 A; 11 C; 14 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Toxoplasma gondii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Toxoplasma oocyst;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       heavy chains and gene library screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 213; 381pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated Toxoplasma gondii nucleic acids used, e.g. infection caused by this microorganism \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-418930/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9932633-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunogenic protein; Toxoplasma gondii protein; oocyst shedding; cat;
                                                                                                                                                     Sequence 500 BP; 118 A; 118 C; 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HESK-) HESKA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 caagettgeggeegegaagaeagatggtgeageeacagt 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gondii infection; enteric apicomplexa oocyst; Cryptosporidium oocyst;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Milhausen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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71.88;
                             47.1%;
76.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
Pred. No. 14;
0; Mismatches
                                Score 21.2;
Pred. No. 14;
                                                                                                                                                         G; 133 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2
                                                                 DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11;
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                                                             20; Length 500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to treat
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RESULT
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                     WPI; 1999-134646/12.
P-PSDB; W95019, W95020.
New D-sorbitol dehydrogenase gene and recombinant protein - useful
                                                                                                                                                  EP897984-A2
                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                              mat_peptide
                                                                                                                                                                                                                                                                                                                                                                           sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gluconobacter suboxydans.
                                                                    (HOFF ) HOFFMANN LA ROCHE & CO AG
                                                                                        21-AUG-1997;
                                                                                                          13-AUG-1998;
                                                                                                                                                                              repeat_unit
                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                         repeat_unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sorbitol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA sequence of sorbitol dehydrogenase (SLDH) and ORF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X21501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X21501 standard; DNA; 3481 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dehydrogenase; SLDH; open reading frame; ORF2; L-sorbose;
                                                 Miyazaki T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                        97EP-0114432
                                                                                                          98EP-0115231.
                                                                                                                                                                                                                                                                                                            /*tag= r
/note= "mature &
684..704
                                                                                                                                                                  2803..2833
/*tag= j
                                                                                                                                                                                  /rpt_type= inverted
/note= "inverted repeat sequence IR2 as possible
/note= "inverted repeat sequence IR2 as possible
    transcription terminator for SLDH gene as
    indicated in the specification"
                                                                                                                                                                                                                                                          684 . . 693
                                                                                                                                                                                                                                                                                                                                                644..2791
                                                                                                                                                                                                                                     2803..2892
                                                                                                                                                                                                                                                                       /rpt_type= inverted
/note= "inverted repeat sequence IR1 as possible
transcription terminator for ORF2 gene as
                                                                                                                                                                                                                                                                                                                                                                                                                 572..2794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               192..572
                                                                                                                                                                                                                                                                                                                                                  /*tag= e
/note=_"signal sequence for SLDH"
                                                                                                                                                                                                                                                                                                                                                                                  /product= "SLDH gene product"
/note= "corresponding protein
                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "putative Shine-Dalgarno (SD) sequence SLDH gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "ORF2 gene product"
/note= "corresponding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "putative Shine-Dalgarno (SD) sequence ORF2 gene"
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177..182
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                                                                                                                                                                                                                                                                                                                          SLDH protein sequence'
                                                                     'n
                                                 Shinjoh
                                                                                                                                                                                                                                                                                                                                                                                   protein sequence shown in W95019"
                                                 ×
                                                Tomiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                               shown
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                                                                                                              RESULT
V15518
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                                                                                                                                                   The present sequence is the hamster oral papilloma virus L1 DNA. The L1 protein and DNA can be used for the diagnosis of papillon virus infectious diseases related to cancer, screening for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This represents the DNA sequence of the SLDH gene encoding a protein with sorbitol dehydrogenase (SLDH) activity. The DNA also encodes an open reading frame (DRP2) product upstream of the SLDH open reading frame, needed for SLDH activity in vivo. Host cells transformed by a vector comprising the SLDH DNA sequence are used for the recombinant expression of the sorbitol dehydrogenase. Recombinant D-sorbitol dehydrogenase is useful for producing L-sorbose from D-sorbitol. L-sorbose is an important intermediate in vitamin C production.
                                                                                                              Sequence 1503 BP; 434 A; 346 C; 337 G; 386 T; 0 other;
                                                                                                                                       antitumour agents and antisense treatment
                                                                                                                                                                                                         Claim 10; Pages 13-14; 17pp; Japanese.
                                                                                                                                                                                                                                   DNA encoding hamster oral papilloma virus protein - useful for, e.g. diagnosing cancer related papilloma virus infections
                                                                                                                                                                                                                                                                                WPI; 1998-186869/17.
P-PSDB; W47224.
                                                                                                                                                                                                                                                                                                                                                                                 06-AUG-1996;
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                                                                                                                                                                                                                                                                                                                                                     06-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                            17-FEB-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hamster oral papilloma virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L1 DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hamster oral papilloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             V15518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       V15518 standard; DNA; 1503 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3481 BP; 674 A; 1018 C; 1001 G; 788
                                                                                                                                                                                                                                                                                                                         (TORA ) TORAY IND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Fig 3A-D; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for production of L-sorbose, an intermediate in vitamin C production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          388 CCAAGCGTGCGGCCCATGAGCATGAATACGCCGC
                                                       Local Similarity
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6 aagcttgcggccgatcaggccgaatatgcggccgcattat 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 ccaagcttgcggccgatcaggccgaatatgcggc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 76.9
26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             screening; antitumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L1 protein; diagnosis; papilloma virus infectious disease;
                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                     96JP-0207143.
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                                                       46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47.18;
76.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       virus L1 DNA.
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                                                    Score 20.8;
Pred. No. 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             agent; antisense treatment;
                                          Mismatches
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                                                                    DB 19;
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                                        12;
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                                                                   Length 1503;
                                          Indels
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                                                                                                                                                                 papilloma
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                                       0;
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                                       Gaps
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                             Stealth virus
                                                                    spongiform encephalopathy; multiple sclerosis; schizophrenia;
manic depression; major depression; personality disorder; autism;
Rett's syndrome; attention deficit; oppositional defiance; aggres
                                                                                                             Prototype Stealth virus clone; atypically structured virus;
vacuolating cytopathic effect; cytopathic virus; virus detection;
malignancy; multiple myeloma; lymphoma; brain tumour; breast cancer;
salivary gland tumour; Alzheimer's disease; Parkinson's disease;
                                                                                                                                                                                     Nucleotide sequence of the genome of Stealth virus clone 313.
                                                                                                                                                                                                                 13-MAR-2000
                                                                                                                                                                                                                                                                        Z36926 standard; DNA; 8907
                                                                                                                                                                                                                                                                                                                                            6474 aaacctgcggctgatcaggatcaaaaggctgatgcatcat 6513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7647 BP; 2102 A; 1703 C; 1894 G; 1948 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; Pages 14-16; 17pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding hamster oral papilloma virus protein - useful for, e.g. diagnosing cancer related papilloma virus infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-186869/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-AUG-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diagnosis; papilloma virus infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hamster oral papilloma virus genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-MAY-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           V15519 standard;
                                                        anorexia nervosa; bulimia; multi-system illness; virus infection; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TORA ) TORAY IND INC
                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                         6 aagcttgcggccgatcaggccgaatatgcggccgcattat 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             screening; antitumour agent; antisense treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  papilloma virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96JP-0207143
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No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                    12;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Length 7647;
                                                                       aggression;
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Best Local S
Matches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          molecular based methods to detect atypically structured viruses, such as Stealth viruses, which are able to induce a vacuolating cytopathic effect (CPE) in tissue culture, and are distinguishable from known cytopathic viruses, by appearance progression and/or host range, or by serological, electron microscopic and/or molecular markers. The products can be used for detecting viruses in patients with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diseases such as a malignancy, e.g. multiple myeloma, lymphoma, brain tumours, breast cancer, salivary gland tumours, Alzheimer's disease, Parkinson's disease, spongiform encephalopathy, multiple sclerosis, schizophrenia, manic depression, major depression, personality disorders, autism, Rett's syndrome, attention deficit, oppositional defiance, aggression, anorexia nervosa, bulimia, a multi-system tillness, an animal illness or an illness in a domestic dog or cat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  z36925-30 represent the nucleotide sequences of prototype Stealth virus clones. The sequences illustrate the type of sequences that can be used to generate probes and to predict antigenic and biologically active products obtainable from a viral isolate, in the methods of the invention. The specification describes tissue culture, serological and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated viruses, used to develop products for detection, prevention and treatment of stealth virus infections \,\cdot\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6014 caccatcggggccgatcaggccgaccatrcagcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The products can be used for detecting Stealth viruses in biological products such as blood products and foods. The products can also be used for developing agents for treating or preventing virus infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 34-37; 50pp; English
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misc_difference
                                                                                                                                                                                                                                            Stealth virus nucleic acid clone, SEQ ID NO:
                                                                                                                                                                                                                                                                                    08-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8907 BP; 2257 A; 2447 C; 2165 G; 2023 T; 15 other;
                                                                                                   misc_difference
                                                                                                                                                            Stealth virus
                                                                                                                                                                                                    Stealth virus;
                                                                                                                                                                                                                                                                                                                                                                   X84323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         caagcttgcggccgatcaggccgaatatgcggcc
                                                                                                                                                                                                                                                                                                                                                                   standard; DNA; 9181 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                  detection; diagnosis; infection; ss
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  8929
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                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.2%;
              "this nucleotide is represented as a * in the specification, and is included to maintain the base numbering given in the specification"
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Pred.
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No. 28;
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                                                                                                            CC invention relates to a method of detecting and characterising a stealth CC virus by reacting a sample suspected of containing a stealth virus with a CC probe from a known stealth virus and sequencing the resultant isolated CC nucleotide. The method comprises the steps of: (a) isolating DNA or RNA CC cells showing a viral cytopathic effect; (b) testing the reactivity of CC cells showing a viral cytopathic effect; (b) testing the reactivity of CC cells solated DNA or RNA with a molecular probe that contains at least 18 CC or more contiguous nucleotides identical to sequence previously CC identified from a stealth virus; and, optionally (c) sequencing the CC isolated DNA or RNA molecules that react with the probe. The method is CC used to detect stealth virus in a biological product, food or in the CC curvicument. The method is also used to evaluate agents for their CC inhibitory or stimulatory effects on stealth virus replication and to CC determine capacity of the virus to recombine with and potentially alter CC the nucleic acid sequences of a cell or bacterium.
                                              Query Match
Best Local
                                Matches
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                                                                                                       Sequence 9181 BP; 2287 A; 2465 C; 2173 G; 2050 T;
                                                                                                                                                                                                                                                                                                                                                                          This sequence represents a Stealth virus nucleic acid clone. The
                                                                                                                                                                                                                                                                                                                                                                                                         Claim 19; Page 49-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel strains of stealth virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-405521/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-DEC-1997;
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caagettgeggeegateaggeegaatatgeggee 38
                                Similarity
25; Conserv
                                Conservative
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                                           46.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "these nucleotides are represented as * in the specification, and are included to maintain the base numbering given in the specification"
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                              1;
                                             Score 20.8;
Pred. No. 2
                              Mismatches
                                              28;
                                                             DB
                                                           20;
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                                                                                                          206 other;
                              Indels
                                                           Length 9181;
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                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         n the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the
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                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q70114/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                     Best Local
                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                     designed which were complementary to the plus strand of the most 5' region of the EK coding sequence (see Q70115-16). Subcloning and sequencing provided a 116 amino acid EK heavy chain. This protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterokinase; EK; heavy chain; light chain; catalytic domain; digestive disorder; cleavage; fusion protein; trypsinogen; trypsin; enzyme; PACE gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6020 caccatcggggccgatcaggccgaccatrcagcc
Rifin 3193 gene; P.falciparum chromosome 2; Rifin protein; mammalian expression plasmid VR1050; DNA vaccine; immunisa
                                       Rifin 3193
                                                                                       229251;
                                                                                                                                                                                                                                                                                    Sequence 41 BP; 12 A; 10 C; 11 G; 8 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                          complementary to the lambda DNA sequence adjacent to the cloning site for the cDNA insertions (see Q70113-14). In addition, primers were
                                                                                                                                                                                                                                                                                                                                                                                                                                      proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid encoding enterokinase activity - and related vectors, host cells, expression products and antibodies are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JAN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q70114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q70114 standard; DNA;
                                                              28-FEB-2000
                                                                                                               Z29251 standard; DNA; 939 BP
                                                                                                                                                                                                                                                                                                          contained regions corresp. to tryptic peptides (see R57295-9).
                                                                                                                                                                                                                                                                                                                                                                                    Nested oligonucleotide primers were synthesised which were
                                                                                                                                                                                                                                                                                                                                                                                                            Example 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1994-249229/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lavallie ER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9416083-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lambda INNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GEMY ) GENETICS INST INC
                                                                                                                                                                        41 GCTTGGACTTAACCAGGCTGAACTTGCGGCCGCATTCT
                                                                                                                                       10
                                                                                                                                                                                       8 gcttgcggccgatcaggccgaatatgcggccgcattat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ٥
                                                                                                                                                                                                                                                                                                                                                                                                                                                in treating digestive disorders and for cleaving fusion
                                                                                                                                                                                                                                     Similarity
                                      gene.
                                                                                                                                                                                                                                                                                                                                                                                                            Page 19;
                                                                                                                                                                                                                        Conservative
                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93US-0005944.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94WO-US00616.
                                                                                                                                                                                                                                                                                                                                                                                                            50pp; English.
                                                                                                                                                                                                                                     45.3%;
71.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВP
                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                                                                                                Score
                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                20.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6053
                                                                                                                                                                                                                                                DΒ
                                                                                                                                                                                                 45
                                                                                                                                                                                                                       11;
                                                                                                                                                                                                                                                15;
                                                                                                                                                                                                                                               Length 41;
  immunisation;
                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                        Gaps
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Best Local S
Matches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 were used to characterise the protein expression from various life cycle stages of P.falciparum. Oligonucleotide primers were used to amplify each selected ORF from chromosome 2 using genomic DNA as template. The purified amplified products were cloned into the mammalian expression plasmid VRID50 to produce DNA vaccines for immunisation. Blood and sera obtained from groups of mice immunised with doses of vaccine was used to identify stage specific expression of Rifin protein by immunofluorescent antibody testing. The method is useful for determination of subcellular localisation of proteins and for the development of antimicrobial
                                      CDS
                                                                                                                                                 Diagnosis; assay; M.bovis;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 939 BP; 365 A; 133 C; 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 13; Page 16; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of microbial, of vaccine, drug of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-APR-1998;
23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   stage specific protein expression; antimicrobial vaccine; antimicrobial drug; IAF; immunofluorescent antibody testi
                                                                                                                                                                                       Sequence encoding Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is the Rifin 3193 gene of chromosome 2. Rifin genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hoffman SL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (USNA ) US
                                                                                                                           Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                   N81768 standard; DNA;
                                                                                                                                                                                                                 29-DEC-1990
                                                                                                                                                                                                                                                                                                                               702
                                                                                                                                                                                                                                                                                           11
                                                                                                                                                                                                                                                                                                                                          2 atccaagcttgcggccgatcaggccgaatatgcggccg 39
                                                                                                                                                                                                                                                                                                                               atccaagcgagctgccggtattgcagattatgctgcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000-086380/07.
                                                                                                                                                                                                                                                                                                                                                                                l Similarity 71.:
27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEC OF NAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              obial, animal and/or human genomic data for identification drug or diagnostic products -
                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carucci DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0082947.
99US-0082947.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US09047
                                               /label=540 AA protein
/note="p81351"
/label=517 AA protein
/note="P81868"
                       /*tag=
                                                                        /*tag=
                                                                                                  Location/Qualifiers
                                  complement (3948..2395)
                                                                                                                                                                                                                                                                                                                                                                                          45.38;
71.18;
                                                                                                                                                                                                                                                                   4260 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunofluorescent antibody testing; ds
                                                                                                                                                    vaccine;
                                                                                                                                                                                                                                                                                                                                                                             Score 20.4; DI
Pred. No. 31;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                             G; 269
                                                                                                                                                    ds
                                                                                                                                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                                                                                                                                                                                                                                             T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                11;
                                                                                                                                                                                                                                                                                                                                                                                                       21;
                                                                                                                                                                                        540 and
                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                        517
                                                                                                                                                                                          AA residue
                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                 0;
  Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ДЬ
                                                                                                                                                                                                                                                                                                                              N80222/c
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          An isolated DNA molecule that consists essentially of the nucleotide sequence that corresponds to the sequence represented by position 3950 about 2390 and from position 3948 through position 238 of N81768 is claimed. Also claimed is a peptide sequence that consists of a 5-40 AA residue sequence that corresponds to a sequence of the 540 AA residue protein (p881351) or the 517 AA residue protein (p881868) coded for by th DNA sequence. The proteins can be used for determining previous
                                                                                                                                                                                                                                                                                                                                                                                 3510 GCGGCAGCGCAGGCGGAACAAGCGGCCGCA 3481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA sequence. The proteins can be used for determining previous immunological exposure of a mammal to M.tuberculosis or M.bovis and for producing a vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant mycobacterial peptide(s) - used in assays for diagnosis of infection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-FEB-1988;
06-FEB-1987;
 02-FEB-1987;
                        01-FEB-1988;
                                                                                                                                                                            Mycobacterium
                                                                                                                                                                                                                                         Sequence of Mycobacterium
                                                                                                                                                                                                                                                                   19-MAR-1991 (first entry)
                                                                                                                                                                                                                                                                                                                   N80222 standard; DNA; 4380 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4260 BP; 733 A; 1332 C; 1481 G; 714 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 2a-2d; 116pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; P81351, P81868.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1988-271136/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shinnick T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-FEB-1988;
                                                 11-AUG-1988
                                                                                                                                                                                                    Antigen; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccines and for producing antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO8806591-A.
                                                                                                                                                                                                                                                                                                                                                                                             12 gcggccgatcaggccgaatatgcggccgca
                                                                                                                                                                                                                                                                                                                                            12
                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Houghten
                                                                                                                                                                            tuberculosis
 87US-0010007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88US-0159667
87US-0019529
                          88WO-US00281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88WO-US00598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLINIC &
                                                                                                               complement
                                                                                                                           /*tag=
                                                                                                                                        192..187
                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                            45.3%;
80.0%;
                                                                                                                                                                                                                                          tuberculosis DNA contg.
                                                                                                               (2398..4101)
                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 20.4;
Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         41
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for
                                                                                                                                                                                                                                                                                                                                                                                                                                                         9;
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6;

Indels

0;

Gaps

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gene encoding

65

Length 4260;

producing

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RESULT 13
V05708/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                Treatment of autoimmune diseases - by administering autoantigen-coated particles or autoantigen-encoding nucleic acid
                                                                                                                                          03-JUN-1997;
03-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis 65 kDa heat shock protein gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3630 GCGGCAGCGCAGGCGGAACAAGCGGCCGCA 3601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The gene was isolated by probing a lambda gt11 expression library of M.tuberculosis DNA with monoclonal antibodies directed against M.tuberculosis specific antigens. The 19kD, 71kD and the 65kD proteins and genes are claimed, and so is a vaccine comprising DNA encoding M.tuberculosis protein in a recombinant vaccine vector. P80216 is
          construct
                                                                                                                                                                               03-JUN-1997;
                                                                                                                                                                                                                             W09746253-A2
                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                     gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   V05708 standard;
                                                                    WPI; 1998-041892/04.
                                                                                                                   (AURA-) AURAGEN INC
                                                                                                                                                                                                       11-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                 22-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                             V05708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4380 BP; 757 A; 1373 C; 1512 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encoded on the complementary strand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; Fig 8; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful for developing reagents treatment of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genes encoding Mycobacterium tuberculosis protein antigens useful for developing reagents for diagnosis, prevention and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Husson RN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (WHIT-) WHITEHEAD INST BIOM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 gcggccgatcaggccgaatatgcggccgca 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                              shock protein; Mt Hsp65; autoimmune disease; immunotherapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1988-235175/33.
DB; P80215, P80216
                                                                                            JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24;
                                                                                          Prayaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Young RA,
                                                                                                                                                                                                                                                                                                                                    rheumatoid arthritis; multiple sclerosis; ds
                                                                                                                                         97US-0019100
96US-0019100
                                                                                                                                                                              97WO-US09427
                                                                                                                                                                                                                                                                            252..1874
                                                                                                                                                                                                                                                 /product= 65 kDa heat shock protein
                                                                                                                                                                                                                                                               /*tag= a
                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA; 4380 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.3%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shinnick TM;
                                                                                           Ramshaw IA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 20.4;
Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Τ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 4380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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CCCCCXXXTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Z46842/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease; (b) delivering the particle into the recipient cell of the mammal; and (c) repeating step (b) until either a reduction in a cytotoxic immune response or a desensitizing immune response is induced in the mammal. Alternatively, step (a) comprises providing a nucleic acid construct comprising a coding sequence for the antigen, operably linked to control elements such that the coding sequence can be transcribed and translated in a recipient cell, and delivering the construct to the recipient cell using a gene gun. The antigen of step (a) is selected from collagen, Mt Hsp65, myelin basic protein, myelin oligodendrocyte glycoprotein, myelin basic protein, myelin oligodendrocyte glycoprotein.
                                                                                                                                                                                                        Disclosure; Page 17-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3630 GCGGCAGCGCAGGCGGAACAAGCGGCCGCA 3601
                                                                                                                                                                                                                                                                                                                                 New semaphorin polypeptides, useful cell physiology modulators and
                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; Y56855.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (EXEL-) EXELIXIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-DEC-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JP11341988-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Semaphorin K1; cellular physiology; neurite outgrowth; neuron; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Semaphorin K1 gene related sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteolipid protein, and epitopes thereof. These antigens mitigenty of the proteon of the protein of the protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a mammal comprises: (a) providing a particle coated with an antigen against which an immune response is mounted in the autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This DNA sequence encodes the 65 kDa heat shock protein (see W44702), designated Mt Hspb5, of Mycobacterium tuberculosis. This protein cross-reacts with a component of articular cartilage, human Hsp60, that is up-regulated in the joints of arthritic patients. It is proventing an autoimmune disease in the component of the proventing an autoimmune disease in the component of the proventing and autoimmune disease in the proventing and autoimmune disease are also and autoimmune disease and autoimmune disease are also and autoimmune disease are also are also are also a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunogen; pharmaceutical; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Z46842 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4380 BP; 757 A; 1371 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sclerosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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80.0%;
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                                                                                                                                                                                               57pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Pred. No. 37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         738 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 19;
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The invention provided isolated human semaphorin K1 polypeptides. The polypeptides, or nucleic acids encoding them, can be used to modulate cellular physiology by modulating semaphorin K1 activity, e.g. semaphorin K1 polypeptide fragments or antisense nucleic acids can be used to

enhance neurite outgrowth from damaged neurons. The polypeptides can also be used as immunogens, reagents for isolating other semaphorins, or as reagents for screening chemical libraries for lead pharmaceutical agents. The nucleic acids can also be used as probes and primers for diagnostic

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RESULT 15
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Best Local
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17-JUL-1997;
10-OCT-1997;
by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigens. The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1818 BP; 543
                                                                                                                                                                                                            New isolated cancer associated nucleic acids and polypeptides - isolated using sera from cancer patients, used to develop products for the diagnosis, monitoring or treatment of cancers
                                                                                                                                                                                                                                                                                                                           Chen Y, Gout I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-JAN-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prostate cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cancer associated antigen; diagnosis; research; treatment; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Colon cancer associated gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X40055 standard;
                                                                                                                                                                                   Claim 67; Page 651-652; 787pp; English.
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                                                                                                                                                                                                                                                                                                                                                     (LUDW-) LUDWIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1998;
                                                                                                                                                                                                                                                                                                             Pfreundschuh M,
                                                                                                                                                                                                                                                                                                                                                                                  11-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                              10-OCT-1997;
10-OCT-1997;
                                                                                                                                                         The invention relates to a method for diagnosing a disorder characterised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    353 CAAGCTAGCAGCCCATCTGTCTGGTTATGAAGCAGAGTTAT 313
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                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0102322.
97US-0896164.
97US-0061599.
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97US-0948705
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Sahin U,
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                                                                                                                                                                                                                                                                                                              O'Hare M, (
Scanlan MJ,
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Pred. No. 40;
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                                                                                                                                                                                                                                                                                                                            Obata Y,
                                                                                                                                                                                                                                                                                                               Stockert
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                                                                                                                                                                                                                                                                                                                              Old LJ;
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88 x CC
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Best Local
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2715 ggtgggggccgaacaggcccaagctgcggcagc 2747
                                                                                                        Sequence 2885 BP;
                                                                                                                                       cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
                                                                                                                            lung cancer.
                                               Local Similarity
nes 25; Conserv
             8 gcttgcggccgatcaggccgaatatgcggccgc
                                              Conservative
                                                                                                         626 A; 901 C;
                                                          44.9%;
75.8%;
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                                                          Score 20.2;
Pred. No. 43
                                               Mismatches
                                                                                                         838 G; 520 T; 0 other;
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Search completed: March 4, Job time: 5659 sec 2001, 12:07:04

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